

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 02:25:09 / Search time 2501 Seconds

(without alignments)
15016.009 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918

Sequence: 1 GAATTCATGAAAAAACCGC.....ATCACCATGCTGAAGCTT 918

Scoring table: IDENTITY NUC
Gapop 10'-0', Gapext 1.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : GenBank1.*
1: gb_ba.*
2: gb_hcg.*
3: gb_in.*
4: gb_on.*
5: gb_ov.*
6: gb_pac.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_scs.*
12: gb_sy.*
13: gb_un.*
14: gb_vt.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pac.*
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26: em_ro.*
27: em_sbs.*
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30: em_hcg_hum.*
31: em_hcg_inv.*
32: em_hcg_other.*
33: em_hcg_mus.*
34: em_hcg_pln.*
35: em_hcg_rod.*
36: em_hcg_mam.*
37: em_hcg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	6 AR139128	AR139128 Sequence
2	916.4	99.8	918	6 AR139129	AR139129 Sequence
3	799.6	87.1	867	6 AR139130	AR139130 Sequence
4	798	86.9	867	6 AR139131	AR139131 Sequence
5	463.8	50.5	801	12 AF027160	AF027160 Synthetic
6	445	48.5	1630	6 AX023365	AX023365 Sequence
7	445	48.5	1630	6 AX023367	AX023367 Sequence
8	414.4	45.1	867	12 AF416910	AF416910 Synthetic
9	369.6	40.3	861	12 AF416909	AF416909 Synthetic
10	361	39.3	450	6 AR139121	AR139121 Sequence
11	359.4	39.2	450	6 AR139120	AR139120 Sequence
12	358.4	39.0	790	10 MAA05051	MAA05051 Mus muscu
13	352	38.3	790	10 MMV124FRG	X97498 M.musculus
14	348.4	38.0	762	6 AX601792	AX601792 Sequence
15	346.2	37.7	864	12 XXU34924	XXU34924 Synthetic
16	345.2	37.6	780	12 SYN1988CF	SYN1988CF Synthetic
17	345.2	37.6	783	6 AR198737	AR198737 Sequence
18	343.6	37.4	786	6 AX601794	AX601794 Sequence
19	343.6	37.4	1848	6 I73512	I73512 Sequence
20	343.6	37.4	1848	12 U06943	U06943 Synthetic
21	342.8	37.3	771	6 AX601793	AX601793 Sequence
22	329	35.8	786	6 AX601796	AX601796 Sequence
23	327.6	35.7	765	12 AF377321	AF377321 Synthetic
24	326	35.5	888	6 AX055802	AX055802 Sequence
25	324.4	35.3	543	6 AR139118	AR139118 Sequence
26	324.4	35.3	543	6 AR139119	AR139119 Sequence
27	321.2	35.0	811	9 AB064067	AB064067 Homo sapi
28	321	34.8	735	6 E13598	E13598 DNA encodin
29	319.8	34.8	1413	6 AX616568	AX616568 Sequence
30	315	34.3	753	6 I08679	I08679 Sequence
31	314.8	34.3	833	9 AB064110	AB064110 Homo sapi
32	314.6	34.3	378	9 HSA555261	HSA555261 Homo sapi
33	313.8	34.2	829	9 AB064118	AB064118 Homo sapi
34	313.6	34.2	376	9 AB021535	AB021535 Homo sapi
35	313.6	34.2	829	9 AB064107	AB064107 Homo sapi
36	313.6	34.2	829	9 AB064108	AB064108 Homo sapi
37	313.4	34.1	379	9 AB021507	AB021507 Homo sapi
38	312.8	34.1	384	9 HSA239336	HSA239336 Homo sapi
39	310.6	33.8	438	9 HSR01127	HSR01127 Homo sapi
40	310.2	33.8	372	9 AB063793	AB063793 Homo sapi
41	309.4	33.7	375	9 HSU08102	U08102 Human immun
42	308.8	33.6	529	9 HSU43759	U43759 Human immun
43	308.8	33.6	796	9 AB064130	AB064130 Homo sapi
44	307.8	33.5	375	9 HSA245275	AJ245275 Homo sapi
45	307.8	33.5	375	9 HSA245276	AJ245276 Homo sapi

ALIGNMENTS

RESULT 1
AR139128
LOCUS AR139128 918 bp DNA
DEFINITION Sequence 13 from patent US 6207153.
ACCESSION AR139128
VERSION AR139128.1 GI:14481624
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 918)
AUTHORS Dan,M.D., Meitzi,P.K. and Kaplan,H.A.
TITLE Antigen Binding fragments that specifically detect cancer cells,
nucleotides encoding the fragments, and use thereof for the
prophylaxis and detection of cancers

JOURNAL Patent: US 6207153-A 13 27-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..918
 BASE COUNT 213 a 240 c 264 g 201 t
 ORIGIN

Query Match 100.0%; Score 918; DB 6; Length 918;
 Best Local Similarity 100.0%; Pred. No. 8,3e-247;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATTCGGATTCGAGTTGCACTGGCTGGTTCCGCTACCGTT 60
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 QY 61 GGGCAGGCGCGATATTGTGTGAAGCAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 120
 DB 61 GGGCAGGCGCGATATTGTGTGAAGCAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 120
 QY 121 AGAGCACCCCTCTCCGAGGGGCACTCAGAGTGTAGAGCACTTAACTAGGCTGGTAC 180
 DB 121 AGAGCACCCCTCTCCGAGGGGCACTCAGAGTGTAGAGCACTTAACTAGGCTGGTAC 180
 QY 181 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240
 DB 181 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240
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 DB 241 GGCATGCCAGACAGATTGAGTGGCACTGGGTCCGGACAGACTTCACTTCAACATCACT 300
 QY 301 AGACTGAGACCTGAGATTTTGGAGTGTATTACTGTACAGAGTATGTAGTCACTCAG 360
 DB 301 AGACTGAGACCTGAGATTTTGGAGTGTATTACTGTACAGAGTATGTAGTCACTCAG 360
 QY 361 ACACCTCAGATCACTTCCGCGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
 DB 361 ACACCTCAGATCACTTCCGCGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
 QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAAGTGGAGTGGCTCCAG 480
 DB 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAAGTGGAGTGGCTCCAG 480
 QY 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGAGGCTCCGAGACTCTCC 540
 DB 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGAGGCTCCGAGACTCTCC 540
 QY 541 TGTGACGCTCTGGAATTCCTTCAGAACTTTGCTATGCACTGGTCCGAGGCTCTA 600
 DB 541 TGTGACGCTCTGGAATTCCTTCAGAACTTTGCTATGCACTGGTCCGAGGCTCTA 600
 QY 601 GGCAGAGGCGTGAAGTGGGTGGCACTTATATCATATGATGAAGCACTAAATACACGA 660
 DB 601 GGCAGAGGCGTGAAGTGGGTGGCACTTATATCATATGATGAAGCACTAAATACACGA 660
 QY 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGCACTTCCAAAGAACCGGATATCTA 720
 DB 661 GACTCCGTGAAGGCGGATTCACATCTCCAGAGCACTTCCAAAGAACCGGATATCTA 720
 QY 721 AAAATGAACAGCTGAACTGAGGACACGCGTGTCTATTACTGTGCGAGAGATCAGAC 780
 DB 721 AAAATGAACAGCTGAACTGAGGACACGCGTGTCTATTACTGTGCGAGAGATCAGAC 780
 QY 781 CTGTGGGTGATATGACCACTACTACGTTGTGAGACTCTGGGGCAAGAGGACACAGGTC 840
 DB 781 CTGTGGGTGATATGACCACTACTACGTTGTGAGACTCTGGGGCAAGAGGACACAGGTC 840
 QY 841 ACCGCTCTCTCAGATCCGAAACAAAACCTGATCAGGAGAAAGATCTGAACATCAACAT 900
 DB 841 ACCGCTCTCTCAGATCCGAAACAAAACCTGATCAGGAGAAAGATCTGAACATCAACAT 900
 QY 901 CACCATTAAGTAAAGCTT 918
 DB 901 CACCATTAAGTAAAGCTT 918

DB 901 CACCATTAAGTAAAGCTT 918

RESULT 2
 AR139129/c 918 bp DNA linear PAT 16-JUN-2001
 LOCUS
 DEFINITION Sequence 15 from patent US 6207153.
 ACCESSION AR139129
 VERSION AR139129.1 GI:14481625
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 918)
 AUTHORS Dan, M.D., Maiti, P.K. and Kaplan, H.A.
 TITLE Antigen binding fragments that specifically detect cancer cells, nucleotides encoding the fragments, and use thereof for the prophylaxis and detection of cancers

JOURNAL Patent: US 6207153-A 15 27-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..918
 BASE COUNT 201 a 265 c 239 g 213 t
 ORIGIN

Query Match 99.8%; Score 916.4; DB 6; Length 918;
 Best Local Similarity 99.9%; Pred. No. 2,3e-246;
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCCTATTCGGATTCGAGTTGCACTGGCTGGTTCCGCTACCGTT 60
 DB 918 GAATTCATGAAAAAACCCTATTCGGATTCGAGTTGCACTGGCTGGTTCCGCTACCGTT 859
 QY 61 GGCAGGCGCGATATTGTGTGAAGCAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 120
 DB 858 GGCAGGCGCGATATTGTGTGAAGCAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAA 799
 QY 121 AGAGCACCCCTCTCCGAGGGGCACTCAGAGTGTAGAGCACTTAACTAGGCTGGTAC 180
 DB 798 AGAGCACCCCTCTCCGAGGGGCACTCAGAGTGTAGAGCACTTAACTAGGCTGGTAC 739
 QY 181 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240
 DB 728 CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 679
 QY 241 GGCATGCCAGACAGATTGAGTGGCACTGGGTCCGGACAGACTTCACTTCAACATCACT 300
 DB 678 GGCATGCCAGACAGATTGAGTGGCACTGGGTCCGGACAGACTTCACTTCAACATCACT 619
 QY 301 AGACTGAGACCTGAGATTTTGGAGTGTATTACTGTACAGAGTATGTAGTCACTCAG 360
 DB 618 AGACTGAGACCTGAGATTTTGGAGTGTATTACTGTACAGAGTATGTAGTCACTCAG 559
 QY 361 ACACCTCAGATCACTTCCGCGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 420
 DB 558 ACACCTCAGATCACTTCCGCGAGGACCAAGGTGAGATCAAAAGAACTGTGGCTGCA 499
 QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAAGTGGAGTGGCTCCAG 480
 DB 498 CCATCTGTCTCTGGCGGTGGCGGTTCCGAGGTGTGATCAAGTGGAGTGGCTCCAG 439
 QY 481 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGGAGGCTCCGAGACTCTCC 540
 DB 438 GTGCACTGTGTGAGTCTGGGGGAGCGTGTCCAGCTGGGAGGCTCCGAGACTCTCC 379
 QY 541 TGTGACGCTCTGGAATTCCTTCAGAACTTTGCTATGCACTGGTCCGAGGCTCTA 600
 DB 378 TGTGACGCTCTGGAATTCCTTCAGAACTTTGCTATGCACTGGTCCGAGGCTCTA 319
 QY 601 GGCAGAGGCGTGAAGTGGGTGGCACTTATATCATATGATGAAGCACTAAATACACGA 660
 DB 318 GGCAGAGGCGTGAAGTGGGTGGCACTTATATCATATGATGAAGCACTAAATACACGA 259

QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACGGGTATCTA 720
 Db 258 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACGGGTATCTA 199
 QY 721 AATATGAACGCCCTGAGAACCTGAGACACGGCTGTCTATTACTGTGGAGAGATCAGAGC 780
 Db 198 AATATGAACGCCCTGAGAACCTGAGACACGGCTGTCTATTACTGTGGAGAGATCAGAGC 139
 QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGGGGCAAGGAGACACGGTC 840
 Db 138 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGGGGCAAGGAGACACGGTC 79
 QY 841 ACCGTCCTCTCAGAGATCCGAAACAAAACCTGATCAGCGAAGAACTTGAACCATCACCAT 900
 Db 78 ACCGTCCTCTCAGAGATCCGAAACAAAACCTGATCAGCGAAGAACTTGAACCATCACCAT 19
 QY 901 CACCATTAAGTGAAGCTT 918
 Db 18 CACCATTAAGTGAAGCTT 1

RESULT 3

AR139130 AR139130 867 bp DNA linear PAT 16-JUN-2001
 LOCUS Definition Sequence 16 from patent US 6207153.
 AR139130
 AR139130.1 GI:14481626

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match 87.1%; Score 799.6; DB 6; Length 867;
 Best Local Similarity 94.0%; Pred. No. 1.6e-213;
 Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCGCTATCGCATCGCAGTTGCACTGGCTGTTGGCTACCGTT 60
 Db 1 GAATTCATGAAAAAACCGCTATCGCATCGCAGTTGCACTGGCTGTTGGCTACCGTT 60
 QY 61 GCGGAGGCCCATATTGTGTTGTTACCGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 120
 Db 61 GCGGAGGCCCATATTGTGTTGTTACCGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 120
 QY 121 AGAGCCACCCCTCTCTGAGGGGCGAGTCAAGAGTGTATTAGACAGTACTTGAAGCTGTATC 180
 Db 121 AGAGCCACCCCTCTCTGAGGGGCGAGTCAAGAGTGTATTAGACAGTACTTGAAGCTGTATC 180
 QY 181 CAGGAGAAACCTGAGCAAGGCTCCAGAGCTCTCACTATGATGATCCACAGGGGCACT 240
 Db 181 CAGGAGAAACCTGAGCAAGGCTCCAGAGCTCTCACTATGATGATCCACAGGGGCACT 240
 QY 241 GGCATGCGCAAGCAGATTCAAGTGGGAGTGGGTCGGGAGACACTTCACTCTCAACATCAGT 300
 Db 241 GGCATGCGCAAGCAGATTCAAGTGGGAGTGGGTCGGGAGACACTTCACTCTCAACATCAGT 300
 QY 301 AGACTGAGCCTGAAGATTTTGGCAGTGAATTAATGTCAGAGTAAGTGAAGTCAACTGAG 360
 Db 301 AGACTGAGCCTGAAGATTTTGGCAGTGAATTAATGTCAGAGTAAGTGAAGTCAACTGAG 360
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Db 361 ACACCTCAGATCACTTTGCGGCGAGGAGCAAGAGTGAAGATCAACGAATGTGGCTGCA 420
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 Db 421 TC-----CGACAG 429
 QY 481 GTGCACTGTGTGAGTCTGCGGAGGCGGTGTCCAGCTTGGAGAGTCCCTGAGACTCTCC 540
 Db 430 GTGCACTGTGTGAGTCTGCGGAGGCGGTGTCCAGCTTGGAGAGTCCCTGAGACTCTCC 489
 QY 541 TGTGCAACCTCTGATATCCCTTCAGAAAGCTTTGCTATGACATGAGGTCCGCAAGCTCTA 600
 Db 490 TGTGCAACCTCTGATATCCCTTCAGAAAGCTTTGCTATGACATGAGGTCCGCAAGCTCTA 549
 QY 601 GGCAGAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAACATTAATTAATCAAGCA 660
 Db 550 GGCAGAGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAACATTAATTAATCAAGCA 609
 QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACGGGTATCTA 720
 Db 610 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAGAAACGGGTATCTA 669
 QY 721 AATATGAACGCCCTGAGAACCTGAGACACGGCTGTCTATTACTGTGGAGAGATCAGAGC 780
 Db 670 AATATGAACGCCCTGAGAACCTGAGACACGGCTGTCTATTACTGTGGAGAGATCAGAGC 729
 QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGGGGCAAGGAGACACGGTC 840
 Db 730 CTGTGGGTGACTATGACCACTACTACGTTTGAACGCTGGGGCAAGGAGACACGGTC 789
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 Db 790 ACCGTCCTCTCAGAGATCCGAAACAAAACCTGATCAGCGAAGAACTTGAACCATCACCAT 849
 QY 901 CACCATTAAGTGAAGCTT 918
 Db 850 CACCATTAAGTGAAGCTT 867

RESULT 4

AR139131/c AR139131 867 bp DNA linear PAT 16-JUN-2001
 LOCUS Definition Sequence 18 from patent US 6207153.
 AR139131
 AR139131.1 GI:14481627

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match 86.9%; Score 798; DB 6; Length 867;
 Best Local Similarity 93.9%; Pred. No. 4.6e-213;
 Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCGCTATCGCATCGCAGTTGCACTGGCTGTTGGCTACCGTT 60
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 QY 61 GCGGAGGCCCATATTGTGTTGTTACCGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 120
 Db 807 GCGGAGGCCCATATTGTGTTGTTACCGCAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 748

REFERENCE 1
 AUTHORS Kufer, P., Zetli, F., Dreier, T., Baerle, P.A. and Borschert, K.
 TITLE Heteromibodies
 JOURNAL Patent: WO 0006605-A 38 10-FEB-2000;
 KUPER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
 BAERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GBS FUER
 BIOMEDIZINIS (DE)
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 BASE COUNT 445 a 410 c 408 g 367 t
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 Best Local Similarity 76.3%; Pred. No. 8.2e-114;
 Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4;

QY 652 TACTACGAGACTCCGTGAAGGCGCCGATTCACCATCTCCAGAGACACTTCAAGAACAG 711
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 DB 636 TACTATGACGACTCCGTGAAGGCGCCGATTCACCATCTCCAGAGACACTTCAAGAACAG 695
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 QY 712 GTGTATCTAAAAATGAACAGCCTGAGAACCTGAGGACACGCGTGTCTATTACTGTGCGAGA 771
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 DB 696 CTGTATCTGCAATGAACAGCCTGAGAGCTGAGGACACGCGTGTATTAATCTGTGCGAAA 755
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 QY 772 GATCAGAGCTGTGGGTGACT-----ATGACCACTACTAGCTTTGAGACGTCGGGGC 825
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 DB 756 GATATGGGGGTGGGAGAGGCTGAGAGACCTTACTACTACTAGATGAGACGTCGGGGC 815
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 QY 826 AAAGGACCAACGCTACCGTCTCTCCTCAGGATCC 858
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 DB 816 CAAGGACCAACGCTACCGTCTCTCCTCAGGATCC 848
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 LOCUS
 DEFINITION Synthetic construct JB-43 recombinant single chain Fv antibody
 derivative mRNA, partial cds.
 ACCESSION AF416910
 VERSION AF416910.1 GI:16033614
 KEYWORDS
 SOURCE
 ORGANISM
 synthetic construct
 artificial sequences.
 1 (bases 1 to 867)
 Bangle, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,
 Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and
 Paul, S.
 Broad distribution and disease association of vasoactive intestinal
 peptide binding and cleaving autoantibodies
 2 (bases 1 to 867)
 Bangle, Y., Li, L., Cavill, D., Gordon, T., Karle, S., Planque, S.,
 Zhou, Y.-X., Taguchi, H., Bhatia, G., Nishiyama, Y., Arnett, F. and
 Paul, S.
 Direct Submission
 Submitted (06-SEP-2001) Pathology and Laboratory Medicine,
 University of Texas-Houston Medical School, 6431 Fannin, Houston,
 TX 77030, USA
 FEATURES
 source location/Qualifiers
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 /db_xref="GI:16033615"
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 misc_feature
 misc_feature

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BASE COUNT 163 a 251 c 254 g 179 t
ORIGIN
Query Match 45.1%; Score 414.4; DB 12; Length 867;
Best Local Similarity 73.9%; Pred. No. 3.3e-105; Indels 45; Gaps 6;
Matches 625; Conservative 0; Mismatches 176;
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1 GAATTTGTTGACGACGCTTCACGACGACCTGCTGTTGCTCCAGGGGAAAGCCACC 60
130 CTCTCTGACAGGCGGACGCTCAGAGTGTAGTACGACCTTACCTGTTACGACGAAA 189
61 CTCTCTGACAGGCGGACGCTCAGAGTGTAGTACGACCTTACCTGTTACGACGAAA 120
190 CTTGCGGAGGCTCCAGGCTCCTCATCTATGATGATCCACAGGCGGACGCTGCGCA 249
121 CTTGCGGAGGCTCCAGGCTCCTCATCTATGATGATCCACAGGCGGACGCTGCGCA 180
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604 AAGGGGCTGAGTGGGTGGAGTTATATCATATGATGAGAGCACTAAATTAATACGACAGC 663
514 AAGGAGCTGAGTGGGTGGAGTTATATCATATGATGAGAGCACTAAATTAATACGACAGC 570
664 TCCGTAAGGCGGATTCACATCTCCAGAGACACTTCCAGAGACGCGGTATCTAAAA 723
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724 ATGAACAGCTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAGAGCACTGAG 783
631 CTGAGCTCTGTGACCGCGGACGAGACGCGGTGATCTACTGTGAGAGAGTGGAGTGGC 690
784 TTGGGTGACTATGACCACTACAGGTTTGGAGCTGTGGGGAAGGAGGAGGAGGAGGAGG 843
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844 GTTCTCTCAGG-----ATCCGAAACAAAATGATCAGCGAAGAGATCTGAACCATCAC 897
748 GTTCTCTCAGGAGATGATCCGCGGAGACCTTTTCCCGGCGGCGGACATCATCATCAC 807
898 CATCAC 903
808 CATCAC 813

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RESULT 9
AF416909
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
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ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
AUTHORS
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MGWIRHGRGGLWIGYIYSGYVTPDKSPVTITVDPSKQPSIKLSVTAADTA
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373. 780
V_region
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Query Match 40.3%; Score 369.6; DB 12; Length 861;
Best Local Similarity 71.9%; Pred. No. 1.3e-92;
Matches 601; Conservative 0; Mismatches 164; Indels 51; Gaps 7;
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Db 11 TCACGAGTCTCCAGCACCCCTGTCTTGTCTCCAGGGGAAAGGCGACCCCTCTCTGCA 70
 QY 140 GGGCCAGTCAAGTGTAGTACGACTTAACTTGGTATCCAGCAAAACCTGGCCAG 199
 Db 71 GGGCCAGTCAAGTGT--TAGCAGCTACTTAACTTGGTATCCAGCAAAACCTGGCCAG 127
 QY 200 CTCGCCAGGCTCTCATCTATGATGATCCACAGGGGCACTGGCATGCGCAGAGTTCA 259
 Db 128 CTCGCCAGGCTCTCATCTATGATGATCCACAGGGGCACTGGCATGCGCAGAGTTCA 187
 QY 260 GTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCACTAGTACCTGGAGCTGAAGATT 319
 Db 188 GTGGCAGTGGGTCCGGGACAGACTTCACTCTCACTCACTAGTACCTGGAGCTGAAGATT 247
 QY 320 TTGCACTGATTACTCTCAGCAGTATGATGATCTCACTCACTAGTACCTGGAGCTGAAGATT 379
 Db 248 TTGCACTGATTACTCTCAGCAGTATGATGATCTCACTCACTAGTACCTGGAGCTGAAGATT 295
 QY 380 GCGGAGGGACCAAGTGGAGATCAAGAACTGTGGCTGACCATCTGTCTTGGCGGTG 439
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 QY 440 GCGGTTCCGAGGTGGTGTGATCAGTGGAGTGGCTTCCAGGTGACCTGGAGTGTG 499
 Db 338 GCGGTTCCGAGGTGGTGTGATCAGTGGAGTGGCTTCCAGGTGACCTGGAGTGTG 397
 QY 500 GGGGAGCGGTGTCAGGCTGGGAGGTCCTGAGACTTCTGAGCTGTGAGCTGTGATTC 559
 Db 398 GCGCAAGACTGTGAAAGCTTCGAGGACCTGTGCTTCACTGATCTGTCTGAGTGTG 457
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 Db 458 CCATCAGCAGTGTAGTACTTACTTGGGGCTGATCCGCCAGCAGCCAGGGAAGGCGCTGG 517
 QY 614 AGTGGGTGGCAGTTATATCATATGATGAAAGCACTAAATCTACGCACTCCGTGAAG 673
 Db 518 AGTGAATGGGTACATCTATTAATCAGTGGGAGCACTTACCAACC---GTCCCTCAGCA 574
 QY 674 GCCGATTCACCATCTCCAGAGCACTTCCAGAAACAGCGGTATCTAAATGAAGCAAGCC 733
 Db 575 GTCCAGTCAACATATCATATGATGAAAGCACTTTCCTGAAAGCTGAGCTTGG 634
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 QY 794 ATGACCACTACTACCGTTTGGAGCTGTGGGCAAAAGGACACAGGTACCGTCTCTCG 853
 Db 692 ACAGCTATGTTACGGGATAGACTTCTGGGCGCAGGGAACCTGTGTACCGTCTCTCG 751
 QY 854 G-----ATCCGAACAATACTGATCAGGAGAAAGATCTGAACCATCAACATCAC 903
 Db 752 GGAGTGCACTCCGCCCAACCTTTTCCCGGGCGCAGATCATCATCACTCAC 807

RESULT 10
 AR139121/c 450 bp DNA linear PAT 16-JUN-2001
 LOCUS Sequence 6 from patent US 6207153.
 DEFINITION AR139121
 ACCESSION AR139121 GI:14481617
 VERSION AR139121.1
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Dan,M.D., Maiti,P.K. and Kaplan,H.A.
 TITLE Antigen binding fragments that specifically detect cancer cells,
 nucleotides encoding the fragments, and use thereof for the
 prophylaxis and detection of cancers
 JOURNAL Patent: US 6207153-A 6 27-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..450

BASE COUNT 105 a 115 c 134 g 96 t
 ORIGIN
 Query Match 39.3%; Score 361; DB 6; Length 450;
 Best Local Similarity 100.0%; Pred. No. 3.4e-90;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATGTGTGAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 129
 Db 73 GATATGTGTGAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 132
 QY 130 CTCTCTGCAAGGCGCAGTCAAGTGTAGTGAAGTACTTAGCTGTGATCCAGAGAA 189
 Db 133 CTCTCTGCAAGGCGCAGTCAAGTGTAGTGAAGTACTTAGCTGTGATCCAGAGAA 192
 QY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGATGATCAGCAGGCGCACTGGCATGCA 249

RESULT 11
 AR139120 450 bp DNA linear PAT 16-JUN-2001
 LOCUS Sequence 4 from patent US 6207153.
 DEFINITION AR139120
 ACCESSION AR139120
 VERSION AR139120.1 GI:14481616
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 450)
 AUTHORS Dan,M.D., Maiti,P.K. and Kaplan,H.A.
 TITLE Antigen binding fragments that specifically detect cancer cells,
 nucleotides encoding the fragments, and use thereof for the
 prophylaxis and detection of cancers
 JOURNAL Patent: US 6207153-A 4 27-MAR-2001;
 FEATURES Location/Qualifiers
 source 1..450
 BASE COUNT 96 a 135 c 115 g 104 t
 ORIGIN
 Query Match 39.2%; Score 359.4; DB 6; Length 450;
 Best Local Similarity 99.7%; Pred. No. 9.5e-90;
 Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATGTGTGAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 129
 Db 73 GATATGTGTGAGCGAGTCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGGCCACC 132
 QY 130 CTCTCTGCAAGGCGCAGTCAAGTGTAGTGAAGTACTTAGCTGTGATCCAGAGAA 189
 Db 133 CTCTCTGCAAGGCGCAGTCAAGTGTAGTGAAGTACTTAGCTGTGATCCAGAGAA 192
 QY 190 CTGGCCAGGCTCCAGGCTCTCATCTATGATGATCAGCAGGCGCACTGGCATGCA 249

Db	193	CCTGGCCAGGCTCCAGGCTCTCTATCTATGTTGCATCCAGAGGCCACTTGGCATGCCA	252
Qy	250	GACAGGTTTCAGTGGCAGTGGGTCCGGGACAGACTTCCTCCATCCATCAGTAGACTGGAG	309
Db	253	GACAGGTCACAGTGGCAGTGGGTCCGGGACAGACTTCCTCCATCCATCAGTAGACTGGAG	312
Qy	310	CCTGAAGATTTTGCAGTGTATTACTGTACAGCAGTATGGTAGCTACCTCAGACACTTCAG	369
Db	313	CCTGAAGATTTTGCAGTGTATTACTGTACAGCAGTATGGTAGCTACCTCAGACACTTCAG	372
Qy	370	ATCATCTTCGGCGGAGGAGCCAGGTTGGAGATCAAAAGAACTGATGCTGACCATCTGC	429
Db	373	ATCATCTTCGGCGGAGGAGCCAGGTTGGAGATCAAAAGAACTGATGCTGACCATCTGC	432
Qy	430	T 430	
Db	433	T 433	
RESULT 12			
LOCUS	MMAJ5051	790 bp	mRNA linear ROD 06-MAY-1998
DEFINITION	Mus musculus VSV-IND neutralising scFv antibody fragment generated from the germine precursor of antibody V124.		
ACCESSION	AJ005051		
VERSION	AJ005051.1 GI:3123634		
KEYWORDS	scFv fragment; V124 antibody.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE	Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	1 Kallinke, U. and Lamarre, A.		
TITLE	In vitro affinity maturation of VSV-specific single-chain Fv antibody fragments		
REFERENCE	Unpublished		
AUTHORS	2 (bases 1 to 790)		
TITLE	Kallinke, U.		
JOURNAL	Direct Submision		
AUTHORS	Submitted (30-MAR-1998) Kallinke U., Institute of Experimental Immunology, Department of Pathology, Schmelzbergstr. 12, 8051		
TITLE	Zuerich, SWITZERLAND		
JOURNAL	Related sequence: X57498.		
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	/strain="BALB/C"		
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	/cell_type="hybridoma"		
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	/note="VSV-IND neutralising scFv fragment"		
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	428..778		
	/note="heavy chain"		
	BASE COUNT 183 a 191 c 234 g 182 t		
	ORIGIN		
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	Beet Local Similarity 71.6%; Pred. No. 1.8e-89;		
	Matches 530; Conservative 0; Mismatches 171; Indels 39; Gaps 3.		
Qy	70	GATATTGGTGAACCCAGCTCCAGGACCCCTGTTGTCTCCAGGGGAAAGACCAAC	129
Db	29	GACATTTGAATCAACAGCTTCATCTCCCTTACGCTGTCTCAGTTGGAGAGAGTTACT	88
Qy	130	CTTCTCTCAGAGGCCAGTCCAGATGTAGTAGCAG-----CTACTTAGCC	174

Db	Accession	Length	Score	E-value	Organism
Db	ATGACGTCCAAAGTCCAGTCAGAGCCCTTTATATATAGTACCAATCAAAAAGAACTACTTGCGCC	18	11.1	0.0001	Mus musculus
Qy	TGTTTCACAGCAGAAACCTTGCCAGGCTCCACAGCTCTCATCTATAGTGTGCATCCACAG	234	175	1e-05	Mus musculus
Db	TGTTTCACAGCAGAAACCAAGGCGAGCTCTTAACACTGCTGATTTACCTGGGATCCACTAGG	208	149	1e-05	Mus musculus
Qy	GCCACTGCGATGCCAGACAGGTTCCAGTGGACAGTGGGTCGGGACACAGCTTCACTCTCAC	294	235	1e-05	Mus musculus
Db	GAATCTGGGGTCCCTGATCCGCTTCCACAGGAGTGATCTGGGACAGATTTCACTCTCAC	268	209	1e-05	Mus musculus
Qy	ATCAGTACACTGAGACCTTGAAATTTTGCACTGTATTACTGTACAGCATATGTAGCTCA	354	295	1e-05	Mus musculus
Db	ATCAGCAGCTGGAAGCTGGAAGACCTTGCAAGTTTATTAACGTACACAAATTAATAGCT	326	269	1e-05	Mus musculus
Qy	CCTGAGACACCTCAGATCACTTTCGGCGGAGGACCAAGGTGGAGTCAACAGAACTGCG	414	355	1e-05	Mus musculus
Db	ATTAACCGTTCCGAGAGGGGACCAAGCTGGAAATTAAGAGTGTGTGT	373	327	1e-05	Mus musculus
Qy	GCTGACCACTGTGTCTCTGCGCGGTGGCGGTTCCGAGGTGTGTGTATCAGTGGAGTGC	474	415	1e-05	Mus musculus
Db	GTGGTTCTGGCGCGGCGGCTCCGAGGTGTGTGTATCAGTGGAGTGC	424	374	1e-05	Mus musculus
Qy	TCCACAGGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	534	415	1e-05	Mus musculus
Db	TCCGATGTGCACTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	484	425	1e-05	Mus musculus
Qy	CTCTCTGTGTGAGCTCTGGAATTTCCCTTCAGAACTTTGTGTGTGTGTGTGTGTGTGT	594	535	1e-05	Mus musculus
Db	CTCTCTGTGTGAGCTCTGGAATTTCCCTTCAGAACTTTGTGTGTGTGTGTGTGTGTGT	544	485	1e-05	Mus musculus
Qy	GCTCTGAGCAAGGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	654	595	1e-05	Mus musculus
Db	GCTCTGAGCAAGGGCTGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	604	545	1e-05	Mus musculus
Qy	TACGCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	714	655	1e-05	Mus musculus
Db	TATGCACTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	664	605	1e-05	Mus musculus
Qy	TATCTAAATAAGAACAGCTGAGACTGAGACAGGCGTCTATTATTCGTGTGTGTGTGT	774	715	1e-05	Mus musculus
Db	TTCCTGCAATAAGAACAGCTGAGACTGAGACAGGCGTCTATTATTCGTGTGTGTGTGT	724	665	1e-05	Mus musculus
Qy	CAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	794	775	1e-05	Mus musculus
Db	GAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT	744	725	1e-05	Mus musculus
RESULT 13	MMV124FRG	790 bp	DNA	linear	ROD 06-MAY-1991
LOCUS	M.musculus V124 antibody VSV-Indiana neutralising scFv fragment.				
DEFINITION	X97498.1 GI:1495715				
ACCESSION	scFv fragment; V124 antibody.				
VERSION	Mus musculus (house mouse)				
KEYWORDS	Mus musculus				
SOURCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
ORGANISM	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
REFERENCE	Kalinke, U., Krebber, A., Krebber, C., Bucher, E., Pluckhuhn, A.,				
AUTHORS	Zinkernagel, R.M. and Hengartner, H.				
TITLE	Monovalent single-chain Fv fragments and bivalent miniantibodies				
JOURNAL	bound to vesicular stomatitis virus protect against lethal				
MEDLINE	infection				
PUBMED	Eur. J. Immunol. 26 (12), 2801-2806 (1996)				
REFERENCE	97131797				
AUTHORS	2 (bases 1 to 790)				
TITLE	Kalinke, U.				
JOURNAL	Direct Submission				
MEDLINE	Submitted (24-Apr-1996) U. Kalinke, Institute of Experimental				
PUBMED	Immunology, Department of Pathology, Schmelzbergstr. 12, 8091				

Zurich, Switzerland
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Best Local Similarity 71.1%; Pred. No. 1.2e-87;
Matches 526; Conservative 0; Mismatches 175; Indels 39; Gaps 3;
QY 70 GATATTGTTGACGAGCTCTCCAGGACCTCTTGTCTTCACAGGGAAGAGCACC 129
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QY 130 CTCTCTGAGGCGCAGTCAAGTGTATAGTACAG-----CTACTTAGCC 174
DB 89 ATGAGCTGCAAGTCCAGTCAAGACCTTTATATATAGTACAAATCAAAAGACTACTGGCC 148
QY 175 TGGTACACAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCACCAAG 234
DB 149 TGGTACACAGAAACAGGAGGAGTCTCTAACTGTATTTACTGGGATCCACTAG 208
QY 235 GCCACTGATGCGCAGACAGTTCAGTGGAGTGGCTCCGGGACAGACTTCACTCTACC 294
DB 209 GAATCTGGGGTCCCTGATGCTTCAAGGAGTGTGAGTGGAGACATTTCACTCTCAC 268
QY 295 ATCAGTAGACTGAGGCTTGAAGATTTTTCAGTGTATTTACTGTACAGATGATGATCTCA 354
DB 269 ATCAGGAGTGTGAAGGCTGAAGACTGGCAGTTTATTTACTGTACAGATATTTACT-- 326
QY 355 CCTCAGACATCAAGTCTTTCGGCGAGAGGACCAAGTGAATCAAAAGCAACTGTG 414
DB 327 -----ATTACAGTTTCGAGGAGGAGACCAAGCTGAAATTAACCTGTGTGT 373
QY 415 GCTGACCATCTGTCTCTGGCGGTGGCGGTTCCGAGAGTGTGATCAGGTGGAGGTGGC 474
DB 374 G-----GTGTTCTGGCGCGCGGCTCCGAGAGTGTGATCCGAGGTGGAGGT 424
QY 475 TCCAGAGTCAAGTGTGAGTCTGGGAGAGGCGTGTCCAGCTGGAGGTCTTGAGA 534
DB 425 TCCGATGTCAAGTGTGAGTCTGGGAGAGGCTTGTAGTCAAGCTGGAAGGTTCCGAGAA 484
QY 535 CTCTCTGTGAGGCTCTGTGATCCCTTCAAGAGCTTTTGATGATGATGAGTGGGCGCCG 594
DB 485 CTCTCTGTGAGGCTCTGTGATCTTCAAGTAAATTTGAAATGTAATGAGTTCTGTGAG 544
QY 595 GCTTATGAGGAGGCTGTGAGTGGTGGCAGTTATATCATATGATGAAAGACTAAATAC 654
DB 545 GCTTCCAGAGAGGAGGCTGTGAGTGTGTGATATATATAGTGTGAGTGTGATCACTTC 604
QY 655 TACGCAAGCTCCGTGAAGGAGGCTTCCAGAGACATTTCCAGAGACAGGAGT 714
DB 605 TATGACAGACAGTGAAGGAGGCTTCCAGATCTCCAGAGACAAATCCCAAGACACCTG 664

RESULT 14
AX601792 762 bp DNA linear PAT 17-FEB-2003
LOCUS AX601792
DEFINITION Sequence 59 from Patent WO02093519.
ACCESSION AX601792
VERSION AX601792.1 GI:28401800
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
Heintges,T., Tessmann,K., Haeusslinger,D. and Artsenko,O.
AUTHORS Human high-affinity antibody fragments for essential proteins of
TITLE the hepatitis-B virus
JOURNAL Patent: WO 02093519-A 59 21-NOV-2002;
Heintges, Tobias (DE)
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Query Match 38.0%; Score 348.4; DB 6; Length 762;
Best Local Similarity 71.4%; Pred. No. 1.2e-86;
Matches 568; Conservative 0; Mismatches 171; Indels 57; Gaps 6;
QY 65 AGCCGATATGTTGTTAGACGAGTCTCCAGGACCTCTTGTCTTCAGGAGGAAAG 124
DB 14 AAGAGAAATGTTGTTAGACGAGTCTCCAGTCCACTCTTGTCTTCAGGAGGAAAG 73
QY 125 CCACCCTCTCTGCGAGGCGCAGTCAAGTGTATAGAGACTTAACTGATCCAGC 184
DB 74 CCACCCTCTCTGCGAGGCGCACTG---GGTAAAGAGACTTCTTAACTGATCCAGC 130
QY 185 AGAAACCTGGCGAGGCTCCAGGCTCTCATCTATGTGTGATCCAGGCGCACTGGCA 244
DB 131 AGAAACCTGGCGAGGCTCCAGGCTCTCATCTATGTATGATGATCCATTAAGGCGCACTGGCA 190
QY 245 TCCAGACAGTTCAGTGTGAGTGGTCCGGAGACATTTCACTCTCAACATCAATAGAC 304
DB 191 TCCAGACAGTTCAGTGTGAGTGGTCCGGAGACATTTCACTCTCAACATCAATAGAC 250
QY 305 TGGAGCTGGAAGATTTTCAAGTGTATTAAGTGTGAGTGTGATGATGATGATGATGATGAT 364
DB 251 TGAAGCTGGAAGATTTTCAAGTGTATTAAGTGTGAGTGTGATGATGATGATGATGATGAT 292
QY 365 CTCAAGTCACTTTCGGCGAGGAGCAAGTGTGATCAAAAGAACTGTGCTGACCAT 424
DB 293 -----CTTTCGGCGAGGAGCAAAAGTGTATCAAAAGTGTGTGT----- 334
QY 425 CTGTCTGTGGGAGGCTTCCGAGAGTGTGATCAAGTGTGATGATGATGATGATGATGATGAT 484
DB 335 GTGTCTGTGGGAGGCTTCCGAGAGTGTGATCAAGTGTGATGATGATGATGATGATGATGAT 394
QY 485 AGCTGTGAGTGTGAGGAGGCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 544
DB 395 AGCTGTGAGTGTGAGGAGGCTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 454
QY 545 CAGCTTGTGAT-----TCCCTTCAGAAAGTTTGTATGATGATGATGATGATGATGATGATGAT 598

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XX 22-MAY-1997; 97MO-US08962.
 PF 22-MAY-1996; 96US-0657449.
 PR (NOVO-) NOVOPHARM BIOTECH INC.
 PA Dan MD, Kaplan HA, Maiti PK;
 PI WPI: 1998-018515/02.
 XX P-PSDB; AAM40070.
 DR Antigen binding fragment from monoclonal antibody, H11 - allows
 PT tumour specific detection and treatment of neoplasia
 PS Example 7; Page 90-91; 126pp; English.

CC This sequence encodes a human H11 monoclonal antibody single chain V
 CC region fragment (H11-scfv) construct which is capable of forming
 CC monomers. This construct is used to determine the ability of H11-scfv
 CC antibody fragments to bind specifically to the C-antigen on cancer cells.
 CC Such antigen binding fragments may be used for treating a patient with
 CC neoplasia. It is especially useful in the detection of lymphomas and
 CC leukemias where the tumour cells bearing the C antigen are circulating
 CC in the patients bloodstream. The polynucleotide sequence may be used as a
 CC primer or a probe and the encoded protein may be used in a vaccine or for
 CC gene therapy. The human monoclonal antibody (Mab), designated H11,
 CC specifically recognises cancerous cells. H11 is specific for
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 CC prostate adenocarcinoma.

SQ Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 other;

Query: Match 100.0%; Score 918; DB 19; Length 918;
 Best Local Similarity 100.0%; Pred. No. 2.5e-224;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 1 GAATTCATGAAAAAACCCTATCGGATCGAGTGGTCACTGGCTGGTTCCTACCGCT 60
 QY 61 GCGCAGCGCGATATGTTGAGCAGAGTCTCCAGGACCCCTGCTTTCTCCAGGGGAA 120
 DB 61 GCGCAGCGCGATATGTTGAGCAGAGTCTCCAGGACCCCTGCTTTCTCCAGGGGAA 120
 QY 121 AAGAGCACCCTCTCTCTGAGGCGCAGTCAAGTGTATGAGAGCTTACCTGCTGATC 180
 DB 121 AAGAGCACCCTCTCTCTGAGGCGCAGTCAAGTGTATGAGAGCTTACCTGCTGATC 180
 QY 181 CAGCAGAAACCTGCGCAGGCTCCAGAGCTCTCATCTATGATGATCCAGGCGCACT 240
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 DB 361 AAGACTGAGGCTGAGATTTTGCAGGTATTACTGTCAAGCAATATGATGATCACTCT 420
 QY 421 CCATCTGTCTCTGCGGTGCGGTTCGGAGGTGTGATCGAGTGAAGTGGTCCAG 480
 DB 421 CCATCTGTCTCTGCGGTGCGGTTCGGAGGTGTGATCGAGTGAAGTGGTCCAG 480
 QY 481 GTGAGCTGTGAGAGTCTGCGGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGATCTCC 540
 DB 481 GTGAGCTGTGAGAGTCTGCGGGAGGCGGTGTCAGGCTGGAGAGTCCCTGAGATCTCC 540

QY 541 TGTGAGCCTCTGATTCCTCTTGAGAACTTTGCTATGCACTGGGTCGCCAGGCTCTA 600
 DB 541 TGTGAGCCTCTGATTCCTCTTGAGAACTTTGCTATGCACTGGGTCGCCAGGCTCTA 600
 QY 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACATACGA 660
 DB 601 GGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGATGAGAGCACTAAATACATACGA 660
 QY 661 GACTCCGTGAGAGGCGCATTCACATCTCCAGAGACATTCACAAACACGGTATATCTA 720
 DB 661 GACTCCGTGAGAGGCGCATTCACATCTCCAGAGACATTCACAAACACGGTATATCTA 720
 QY 721 AAAATGAACAGCTTGAAGATGAGACACGGTGTCTATTACTGTCCAGAGATCAGAGC 780
 DB 721 AAAATGAACAGCTTGAAGATGAGACACGGTGTCTATTACTGTCCAGAGATCAGAGC 780
 QY 781 CTGTTGGGTGATATGACCACTACTACAGGTTTGAAGCTGGGGCAAGGGACACAGGTC 840
 DB 781 CTGTTGGGTGATATGACCACTACTACAGGTTTGAAGCTGGGGCAAGGGACACAGGTC 840
 QY 841 ACCGTCTCTCAGATTCGGAACAAAACCTGATCAGCGAAGAGATCTGAACCATCACCAT 900
 DB 841 ACCGTCTCTCAGATTCGGAACAAAACCTGATCAGCGAAGAGATCTGAACCATCACCAT 900
 QY 901 CACCATTTAGTGAAGCTT 918
 DB 901 CACCATTTAGTGAAGCTT 918

RESULT 2
 AAD04537
 ID AAD04537 standard; DNA; 918 BP.
 AC AAD04537;
 XX 04-JUL-2001 (first entry)

DE Human monoclonal antibody H11-single chain variable region (scfv) DNA #1.
 XX
 XX Human; monoclonal antibody; Mab; H11; single chain variable region; scfv;
 KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
 KW C-antigen; chronic leukaemia; glioma; ds.

OS Homo sapiens.

XX Key Location/Qualifiers

FT 1..918
 FT CDS
 FT /tag= a
 FT /product= "Human H11-single chain variable region (scfv)"
 FT /transl_except= (pos:904..915, aa:His-Lys)
 FT /note= "insertion of two inframe stop codon alters the
 FT reading frame; CDS does not include start and stop
 FT codons"
 FT /partial
 FT 430..474
 FT misc_feature
 FT /tag= b
 FT /note= "Encodes (SGGG)3 linker sequence"

XX US6207153-B1.

XX 27-MAR-2001.

XX 22-MAY-1997; 97US-0862124.

XX 22-MAY-1996; 96US-0657449.

XX (VIVE-) VIVENTIA BIOTECH INC.

XX Dan MD, Maiti PK, Kaplan HA;

DR WPI, 2001-289584/30.
 DR P-PSDB; AAE00947.
 PT Composition comprising antigen binding fragments of an antibody that
 PT recognizes an antigen on neoplastic cells but not on normal cells for
 PT use in diagnosis, imaging and treatment of carcinomas -
 XX
 XX Example 7; Column 61-64; 56bp; English.
 CC The present DNA sequence encodes human monoclonal antibody (Mab), H11-
 CC single chain variable region (scFv). The H11 light chain variable region
 CC is linked to the heavy chain variable region through a (GGGGG)3 linker to
 CC form monomers.
 CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)
 CC single chain variable (V) region fragment and their corresponding DNA
 CC molecules. H11 antibody is an immunoglobulin of IgM subclass which is
 CC specific to C-antigen found specifically on neoplastic cells and not on
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused
 CC to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.
 CC A pharmaceutical composition comprising H11 and its derivatives are
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma, small
 CC cell lung carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas
 CC and chronic leukaemias. H11 DNA is also used in vaccines and gene
 CC therapy.
 XX
 XX Sequence 918 BP; 213 A; 240 C; 264 G; 201 T; 0 other;
 S0
 Query Match 100.0%; Score 918; DB 22; Length 918;
 Best Local Similarity 100.0%; Pred. No. 2,5e-224;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCGCTATCGCGATCGAGTTGACATGCGTGGTTGGTACCGCTT 60
 DB 1 GAATTCATGAAAAAACCGCTATCGCGATCGAGTTGACATGCGTGGTTGGTACCGCTT 60
 QY 61 GCGGAGGCCCATATTTGTTTGAACGACATCCAGGACCCCTGTTTCTCCAGGGGAA 120
 DB 61 GCGGAGGCCCATATTTGTTTGAACGACATCCAGGACCCCTGTTTCTCCAGGGGAA 120
 QY 121 AGAGCCACCCCTCTCTGACAGGGGCGATGAGTGTAGTAGCAGTACTTACCTGTGATC 180
 DB 121 AGAGCCACCCCTCTCTGACAGGGGCGATGAGTGTAGTAGCAGTACTTACCTGTGATC 180
 QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGATGATCCAGGAGGCACT 240
 DB 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGATGATCCAGGAGGCACT 240
 QY 241 GGCATGCCAGACAGTTCAGTGGCAATGGGTCGGGACAGACTTCACTCTACCATCACT 300
 DB 241 GGCATGCCAGACAGTTCAGTGGCAATGGGTCGGGACAGACTTCACTCTACCATCACT 300
 QY 301 AGACTGGAGGCTGAAGATTTTGGAGTGTATCTGTGACAGTATGATGATGATGATGAT 360
 DB 301 AGACTGGAGGCTGAAGATTTTGGAGTGTATCTGTGACAGTATGATGATGATGATGAT 360
 QY 361 ACACCTCAGATCACTTTCCGCGAGGAGCAAGGTGAGATCAACGAACTGTGGCTGCA 420
 DB 361 ACACCTCAGATCACTTTCCGCGAGGAGCAAGGTGAGATCAACGAACTGTGGCTGCA 420
 QY 421 CCATCTGTCTTGGCGGTGGGCTTCCGAGAGTGTGATCAAGTGGAGGTGGCTCCAG 480
 DB 421 CCATCTGTCTTGGCGGTGGGCTTCCGAGAGTGTGATCAAGTGGAGGTGGCTCCAG 480
 QY 481 GTGAGAGTGTGATGTGGGAGGAGCGTGTCCAGCTGGGAGGTCCCTGAGACTCTCC 540
 DB 481 GTGAGAGTGTGATGTGGGAGGAGCGTGTCCAGCTGGGAGGTCCCTGAGACTCTCC 540
 QY 541 TGTGACAGCTTGTGATTCCTTTCAGAACTTTGTATGACATGGGTCCGACAGCTCTA 600
 DB 541 TGTGACAGCTTGTGATTCCTTTCAGAACTTTGTATGACATGGGTCCGACAGCTCTA 600

DB 541 TGTGACAGCTTGTGATTCCTTTCAGAACTTTGTATGACATGGGTCCGACAGCTCTA 600
 QY 601 GGCAGAGGGGCTGAGTGGGTGGAGCTATATCATATGATGAGACACTAAATATCAAGCA 660
 DB 601 GGCAGAGGGGCTGAGTGGGTGGAGCTATATCATATGATGAGACACTAAATATCAAGCA 660
 QY 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCAGAAACACGGTGTATCTA 720
 DB 661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACATTCAGAAACACGGTGTATCTA 720
 QY 721 AAATGAACAGCTGAGAACATGAGGACACGGCTGTCTATTACTGTGAGAGATCAAGC 780
 DB 721 AAATGAACAGCTGAGAACATGAGGACACGGCTGTCTATTACTGTGAGAGATCAAGC 780
 QY 781 CTGTGGGTGACATATGACCACTACTACGATTTGACGCTGGGCAAGGACACCGGTC 840
 DB 781 CTGTGGGTGACATATGACCACTACTACGATTTGACGCTGGGCAAGGACACCGGTC 840
 QY 841 ACCGCTCTCTCAGGATCCGAAACAAACCTGATCAGCGAAGATCTGAACCATCACCAT 900
 DB 841 ACCGCTCTCTCAGGATCCGAAACAAACCTGATCAGCGAAGATCTGAACCATCACCAT 900
 QY 901 CACCATTAAGTGAAGCTT 918
 DB 901 CACCATTAAGTGAAGCTT 918

RESULT 3
 AAD04538/c
 ID AAD04538 standard; DNA, 918. BP.
 XX
 XX AAD04538;
 AC
 DT 04-JUL-2001 (first entry)
 XX
 XX Human H11-single chain variable region (scFv) complementary DNA #1.
 DE
 XX Human; monoclonal antibody; Mab; H11; single chain variable region; scFv;
 KW neoplastic disease; melanoma; immunoglobulin IgM; gene therapy; lymphoma;
 KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
 KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
 KW C-antigen; chronic leukaemia; glioma; ds.
 XX
 XX Homo sapiens.
 OS
 XX US6207153-B1.
 PN
 XX 27-MAR-2001.
 PD
 XX 22-MAY-1997; 97US-0862124.
 PF
 XX 22-MAY-1996; 96US-0657449.
 PR
 XX (VIVE-) VIVENTIA BIOTECH INC.
 PA
 XX Dan MD, Malti PK, Kaplan HA;
 PI
 XX WPI: 2001-289584/30.
 DR
 XX WPI: 2001-289584/30.
 XX
 XX Example 7; Column 65-66; 56bp; English.
 PS
 XX The present sequence is human monoclonal antibody (Mab), H11-single chain
 CC variable region (scFv) complementary DNA.
 CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)
 CC single chain variable (V) region fragment and their corresponding DNA
 CC molecules. H11 antibody is an immunoglobulin of IgM subclass which is
 CC specific to C-antigen found specifically on neoplastic cells and not on
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused

CC to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.
 CC A pharmaceutical composition comprising H11 and its derivatives are
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,
 CC lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas
 CC and chronic leukaemias. H11 DNA is also used in vaccines and gene
 CC therapy.

xx Sequence 918 BP; 201 A; 265 C; 239 G; 213 T; 0 other;

Query Match 99.8%; Score 916.4; DB 22; Length 918;

Best Local Similarity 99.9%; Pred. No. 6.5e-224;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAAGCGCTATCGCATGCGATTGCACTGGCTGGTTGCGTACCGTT 60
 DB 918 GAATTCATGAAAAAAGCGCTATCGCATGCGATTGCACTGGCTGGTTGCGTACCGTT 859
 QY 61 GGGCAGGCGCGATATGTTGTGAAGCAGTCTCCAGAGCACTGCTTTGTCTCCAGGGGAA 120
 DB 858 GGGCAGGCGCGATATGTTGTGAAGCAGTCTCCAGAGCACTGCTTTGTCTCCAGGGGAA 799
 QY 121 AGAGCCACCCCTCTCTGCAAGGCGCACTCAGAGTGTATGAGCACTTACTTACCTGTGAC 180
 DB 798 AGAGCCACCCCTCTCTGCAAGGCGCGCATCAGAGTGTATGAGCACTTACTTACCTGTGAC 739
 QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATGATCCAGGCGCACT 240
 DB 738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGATGATGATCCAGGCGCACT 679
 QY 241 GGCATGCCAGAGAGTTCAGTGGAGTGGGTCCGGGACAGACTTCACTCCACCATCACT 300
 DB 678 GGCATGCCAGAGAGTTCAGTGGAGTGGGTCCGGGACAGACTTCACTCCACCATCACT 619
 QY 301 AGACTGAGGCTGAGATTTTCAGTGTATTACTGTCAAGCATATGATGATCACTCACTCAG 360
 DB 618 AGACTGAGGCTGAGATTTTCAGTGTATTACTGTCAAGCATATGATGATCACTCACTCAG 559
 QY 361 ACACCTCAGATCACTTTGGCGGAGGAGCAAGTGGAGATCAAAAGAACTGTGCTGCA 420
 DB 558 ACACCTCAGATCACTTTGGCGGAGGAGCAAGTGGAGATCAAAAGAACTGTGCTGCA 499
 QY 421 CCATGCTCTCTGGGGGTGGCGGTTCCGAGGTGGTGGATCAAGTGGAGTGGTCCGAG 480
 DB 498 CCATGCTCTCTGGGGGTGGCGGTTCCGAGGTGGTGGATCAAGTGGAGTGGTCCGAG 439
 QY 481 GTGCACTGTGTGAGTCTGTGGGAGGCGGTGTCAGAGCTGGAGAGTCCCTGAGACTCTCC 540
 DB 438 GTGCACTGTGTGAGTCTGTGGGAGGCGGTGTCAGAGCTGGAGAGTCCCTGAGACTCTCC 379
 QY 541 TGTGCAAGCTCTGTGATTTCCCTTCAAGAGCTTTGCTATGCACTGGGTCCGAGGCTCTA 600
 DB 378 TGTGCAAGCTCTGTGATTTCCCTTCAAGAGCTTTGCTATGCACTGGGTCCGAGGCTCTA 319
 QY 601 GGCAGAGGGGCTGAGAGTGGGTGGCAGTTATATATATGAGGAAGCACTAAATACACGA 660
 DB 318 GGCAGAGGGGCTGAGAGTGGGTGGCAGTTATATATATGAGGAAGCACTAAATACACGA 259
 QY 661 GACTCCGTGAAAGGCGGATTCACCATCTTCAGAGACACTTCCAGAAACAGGCTGTATCTA 720
 DB 258 GACTCCGTGAAAGGCGGATTCACCATCTTCAGAGACACTTCCAGAAACAGGCTGTATCTA 199
 QY 721 AAAATGAACAGCTGAGAACTGAGGACACGCGTGTCTATTAATGTCGAGAGATCAGAGC 780
 DB 198 AAAATGAACAGCTGAGAACTGAGGACACGCGTGTCTATTAATGTCGAGAGATCAGAGC 139
 QY 781 CTGTTGGGAGTATGACCACTACATACGTTTGGAGTGTGGGGGAAAGGACACAGGTC 840
 DB 138 CTGTTGGGAGTATGACCACTACATACGTTTGGAGTGTGGGGGAAAGGACACAGGTC 79
 QY 841 ACCGTCCTCCTGAGATCCGAAACAAAACATGATCAGGAAAGATCTGAACATCAACAT 900

DB 78 ACCGTCCTCCTGAGATCCGAAACAAAACATGATCAGGAAAGATCTGAACATCAACAT 19
 QY 901 CACCATTTGTGAAAGCTT 918
 DB 18 CACCATTTGTGAAAGCTT 1

RESULT 4

AAV10119 standard; DNA; 867 BP.

AAV10119;

29-MAY-1998 (first entry)

Human H11-scFv construct dimer forming DNA sequence.

H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;

V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;

primer; vaccine; gene therapy; glioblastoma; neuroblastoma;

malignant melanoma; adenocarcinoma; small cell lung carcinoma;

single chain variable region; scFv; ss.

Synthetic.

Homo sapiens.

Key

CDS

1..867

/tag= a

/product= H11-scFv construct

/note= "partial sequence of dimer forming

construct is interrupted by an intron."

intron

856..861

/tag= b

WO9744461-A2.

27-NOV-1997.

22-MAY-1997; 97WO-US08962;

22-MAY-1996; 96US-0657449.

(NOVO-) NOVOPIRAM BIOTECH INC.

Dan MD, Kaplan HA, Maiti PK;

WPI; 1998-018515/02.

P-PSDB; AAM40071.

Antigen binding fragment from monoclonal antibody, H11 - allows

tumour specific detection and treatment of neoplasia

Example 7; Page 94-95; 126pp; English.

This sequence encodes a human H11 monoclonal antibody single chain V

region fragment (H11-scFv) construct which is capable of forming

dimers. This construct is used to determine the ability of H11-scFv

antibody fragments to bind specifically to the C-antigen on cancer cells.

Such antigen binding fragments may be used for treating a patient with

neoplasia. It is especially useful in the detection of lymphomas and

leukaemias where the tumour cells bearing the C antigen are circulating

in the patients bloodstream. The polynucleotide sequence may be used as a

primer or a probe and the encoded protein may be used in a vaccine or for

gene therapy. The human monoclonal antibody (Mab), designated H11,

specifically recognises cancerous cells. H11 is specific for

glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,

lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and

prostate adenocarcinoma.

Sequence 867 BP; 209 A; 229 C; 241 G; 188 T; 0 other;


```

Db      1 GAATTCATGAAAAAACCCTATCGCGATCGCAGTTGCACTGCGTGTTCGTAACGTT 60
QY      61 GGGGAGGCGGATATGTTGATGAGCTCCAGGACCGCTGTTGTTCTCCAGGGGAA 120
Db      61 GGGGAGGCGGATATGTTGATGAGCTCCAGGACCGCTGTTGTTCTCCAGGGGAA 120
QY      121 AGAGCCACCTCTCTCGCAGAGGCGCAGTCAAGAGTTAGTAGCACTACTAGCTGTAC 180
Db      121 AGAGCCACCTCTCTCGCAGAGGCGCAGTCAAGAGTTAGTAGCACTACTAGCTGTAC 180
QY      181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGGCCACT 240
Db      181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGGCCACT 240
QY      241 GGCATGCCAGAGAGTTGAGTGGGTCCGGGAGAGCTTCCTCCTCACCACCTCACT 300
Db      241 GGCATGCCAGAGAGTTGAGTGGGTCCGGGAGAGCTTCCTCCTCACCACCTCACT 300
QY      301 AGACTGAGCCTGAAAGATTTTGAGTATTAATCTGTCAGCAGATGTTAGTCACTCAG 360
Db      301 AGACTGAGCCTGAAAGATTTTGAGTATTAATCTGTCAGCAGATGTTAGTCACTCAG 360
QY      361 AGACTCAGATCACTTTGCGCGAGGAGCCAGGTGAGATCAACGAACTGTGCTGCA 420
Db      361 AGACTCAGATCACTTTGCGCGAGGAGCCAGGTGAGATCAACGAACTGTGCTGCA 420
QY      421 CCATCTGTCTGCGCGGTGCGGTTCCGAGGTTGATGATGAGAGTGGTCCGACG 480
Db      421 TC-----CGACGAG 429
QY      481 GTGCACTGTGAGTCTGCGGAGGCGGTGTCAGCCTGGAAGTCCCTGAGACTTCC 540
Db      430 GTGCACTGTGAGTCTGCGGAGGCGGTGTCAGCCTGGAAGTCCCTGAGACTTCC 489
QY      541 TGTGCACTGTGAGTCTGCGGAGGCGGTGTCAGCCTGGAAGTCCCTGAGACTTCC 600
Db      490 TGTGCACTGTGAGTCTGCGGAGGCGGTGTCAGCCTGGAAGTCCCTGAGACTTCC 549
QY      601 GSCAAGGCGCTGAGTGGGTGAGTATATCATATGATGAGGACCTAAATATCAACGA 660
Db      550 GSCAAGGCGCTGAGTGGGTGAGTATATCATATGATGAGGACCTAAATATCAACGA 609
QY      661 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAACGCGTGTATCTA 720
Db      610 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAACGCGTGTATCTA 669
QY      721 AAAATGAACGCTGAGAACTGAGACAGCGCTGTATTACTGTGCGAGATCAAGAC 780
Db      670 AAAATGAACGCTGAGAACTGAGACAGCGCTGTATTACTGTGCGAGATCAAGAC 729
QY      781 CTGTTGGGTGACTATGACCACTACTACGCTTGGAGCTGTGGGGCAAGGAGCAAGGTC 840
Db      730 CTGTTGGGTGACTATGACCACTACTACGCTTGGAGCTGTGGGGCAAGGAGCAAGGTC 789
QY      841 ACCGTCTCTCAGATCCGAAACAAACTGATCAAGGAAAGATCTGAACCATCAACAT 900
Db      790 ACCGTCTCTCAGATCCGAAACAAACTGATCAAGGAAAGATCTGAACCATCAACAT 849
QY      901 CACCATTAAGTAAGCTT 918
Db      850 CACCATTAAGTAAGCTT 867

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RESULT 6

AA04540/c
 ID AA04540 standard; DNA, 867 BP.

XX AA04540;

XX 04-JUL-2001 (first entry)

XX Human H11-single chain variable region (scfv) complementary DNA #2.

```

KW Human; monoclonal antibody; Mab; H11; single chain variable region; scfv;
KW neoplastic disease; melanoma; immunoglobulin IGM; gene therapy; lymphoma;
KW carcinoma; breast; lung; gastric; prostate; ovary; colon; lung; vaccine;
KW neuroblastoma; soft tissue sarcoma; prostatic adenocarcinoma; cytostatic;
KW C-antigen; chronic leukemia; glioma; ds.
XX
OS Homo sapiens.
XX
PN US6207153-B1.
XX
PD 27-MAR-2001.
XX
PF 22-MAY-1997; 97US-0862124.
XX
PR 22-MAY-1996; 96US-0657449.
XX
PA (VIVE-) VIVENTIA BIOTECH INC.
XX
PI Dan MD, Maiti PK, Kaplan HA;
XX
DR MPI; 2001-289584/30.
XX
PS Example 7; Column 71-72; 56bp; English.
XX
PT Composition comprising antigen binding fragments of an antibody that
PT recognizes an antigen on neoplastic cells but not on normal cells for
PT use in diagnosis, imaging and treatment of carcinomas
XX
The present sequence is human monoclonal antibody (Mab), H11-single chain
CC variable region (scfv) complementary DNA.
CC The invention relates to human monoclonal antibody (Mab) H11, (scfv)
CC single chain variable (V) region fragment and their corresponding DNA.
CC molecules. H11 antibody is an immunoglobulin of IGM subclass which is
CC specific to C-antigen found specifically on neoplastic cells and not on
CC normal cells. H11 is an antibody obtained from the fusion of peripheral
CC blood lymphocytes of a 64 year old male with a low grade glioma and fused
CC to a human myeloma cell line to produce a hybridoma designated NBGM1/H11.
CC A pharmaceutical composition comprising H11 and its derivatives are
CC useful in the diagnosis, imaging and treatment of neoplastic disease,
CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian
CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,
CC lymphoma, neuroblastoma, glioma, soft tissue sarcoma, small
CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas
CC and chronic leukemias. H11 DNA is also used in vaccines and gene
XX therapy.
SQ Sequence 867 BP, 189 A, 241 C, 229 G, 208 T, 0 other;
XX
Query Match 86.9%; Score 798; DB 22; Length 867;
Best Local Similarity 93.9%; Pred. No. 1e-193;
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1,
QY 1 GAATTCATGAAAAAACCCTATGCGATGCGAGTTGCACTGCGTGTTCGTAACGTT 60
Db 867 GAATTCATGAAAAAACCCTATGCGATGCGAGTGCATCGCTGTTGCTAACGTT 808
QY 61 GCGCAGGCGGATATGTTGATGAGCTCCAGGACCGCTGTTGTTCTCCAGGGGAA 120
Db 807 GCGCAGGCGGATATGTTGATGAGCTCCAGGACCGCTGTTGTTCTCCAGGGGAA 748
QY 121 AGAGCCACCTCTCTCGCAGAGGCGCAGTCAAGAGTTAGTAGCACTACTAGCTGTAC 180
Db 747 AGAGCCACCTCTCTCGCAGAGGCGCAGTCAAGAGTTAGTAGCACTACTAGCTGTAC 688
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGGCCACT 240
Db 687 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGTCATCCAGGGCCACT 628
QY 241 GGCATGCCAGAGAGTTGAGTGGGTCCGGGAGAGCTTCCTCCTCACCACCTCACT 300
Db 627 GGCATGCCAGAGAGTTGAGTGGGTCCGGGAGAGCTTCCTCCTCACCACCTCACT 568
QY 301 AGACTGAGCCTGAAAGATTTTGAGTATTAATCTGTCAGCAGATGTTAGTCACTCAG 360

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D	b		567	AACCTGAGACCCTGGAAATTTTGTGAGTGATTAATGTTCACAGAGATAGTAGCTCAACTCAG	508
O	y		361	ACAACCTCAGATCACTTTCCGCCGAGAGACCAACGTGAGATCAAAGAACTGTGGCTGCA	420
D	b		507	ACACCTCAGATCATCTTTCCGCCGAGAGAACCAAGTGGAGATCAACGAATGTGGCTGCA	448
O	y		421	CCATCTGTCTCTGGCCGATGGCGTTCCGAGAGTGTGATCAGGTGAGGTGCCCTCCAG	480
D	b		447	TC-----CGAGCAG	439
O	y		481	GTCAGACTGTGGAGTCTGGGGGAGGCCTGTGTCCAGCTCGAGAGTCCCTGAGACTTCC	540
D	b		438	GTCGACCTGTGGAGTCTGGGGGAGGCCTGTGTCCAGCTCGAGAGTCCCTGAGACTTCC	379
O	y		541	TGTGAGCCTCTGGATTCCCCTTCAGAAGCTTGTCTATGATGCACTGGTCCGCCAGCTCTA	600
D	b		378	TGTGAGCCTCTGGATTCCCCTTCAGAAGCTTGTCTATGATGCACTGGTCCGCCAGCTCTA	319
O	y		601	GGCAAGGGGCTGGAGTGGGTGGCATTTATATCATATGATGAAGCATTAATACTACGCA	666
D	b		318	GGCAAGGGGCTGGAGTGGGTGGCATTTATATCATATGATGAAGCATTAATACTACGCA	259
O	y		661	GACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACACTTCCAAAGAACCCGGGTATCTA	720
D	b		258	GACTCCGTGAAGGGCCGATTCAACATCTCCAGAGACACTTCCAAAGAACCCGGGTATCTA	199
O	y		721	AAATGAAACAGCCTGGAAGTGAAGACACGCGCTGTCTATTACTGTGCGAGATCAGAGC	780
D	b		198	AAATGAAACAGCCTGGAAGTGAAGACACGCGCTGTCTATTACTGTGCGAGATCAGAGC	139
O	y		781	CTGTTGGGTGACTATGACCACTATCTACGGTTTTGGACGTCTGGGGCAAAAGGACACAGTC	840
D	b		138	CTGTTGGGTGACTATGACCACTATCTACGGTTTTGGACGTCTGGGGCAAAAGGACACAGTC	79
O	y		841	ACCGTCTCTCAGAGATCCGAAACAAAACGTGATGAGGAAGATCTGAACCATCACCAT	900
D	b		78	ACCGTCTCTCAGAGATCCGAAACAAAACGTGATGAGGAAGATCTGAACCATCACCAT	19
O	y		901	CACCATTAAGTGAAGCTT	918
D	b		18	CACCATTAAGTGAAGCTT	1
<hr/>					
RESULT 7					
AAZ50587					
ID	AAZ50587 standard; DNA; 1630 BP.				
AC	AAZ50587;				
XX					
DT	23-MAY-2000 (first entry)				
XX					
DE	HD70scFv-CH1-GM-CSF chain encoding DNA.				
XX					
KM	HD70; single-chain variable fragment; scFv; 17-1A antigen; human;				
KM	EpCAM; epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;				
KM	granulocyte/macrophage colony stimulating factor; heteromibody;				
KM	CHI-domain; multifunctional compound; heavy chain constant domain;				
KM	immunoglobulin; cytostatic; immunostimulatory; antileukemia; diagnosis;				
KW	antiproliferative; prevention; treatment; malignant; haematopoietic cell;				
KX	lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; de.				
OS	Homo sapiens.				
XX					
FH	Key				
FT	CDS				
FT	misc_feature				
FT	label= HD70_scFv				
PN	WO200006605-A2.				

XX 10-FEB-2000.
 PD 28-JUL-1999; 99WO-EP05416.
 XX 28-JUL-1998; 98EP-0114082.
 XX PR 28-JUL-1998; 98EP-0114082.
 XX XX
 XX (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
 PA Kufer P, Dreier T, Baerle PA, Borschert K, Zettl F;
 PI MPI: 2000-195265/17.
 DR P-PSDB; AAY44994.
 XX
 XX New multifunctional compounds useful for preventing and/or treating
 PT malignant cell growth and for detection and diagnosis
 PT
 PS Claim 8; Fig 55A; 16pp; English.
 XX
 XX The patent discloses heteromimibodies which are multifunctional compounds
 CC producible in a mammalian host cell as a secretable and fully functional
 CC heterodimer of two polypeptide chains, where one of the polypeptide
 CC chains comprises: a CH1-domain (constant domain of an immunoglobulin
 CC heavy chain) and the other chain comprises C₁-domain (constant domain of
 CC an immunoglobulin light chain). The polypeptide chains further comprise,
 CC fused to the constant domains at least two (poly)peptides having
 CC different receptor or ligand functions, where further at least two of the
 CC different (poly)peptides lack an intrinsic affinity for one another and
 CC are linked via the constant domains. The heteromimibodies have
 CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
 CC activities. These compounds can be used for diagnosing, preventing and
 CC treating malignant cell growth related to malignancies of haematopoietic
 CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
 CC melanomas and sarcomas.
 CC The present sequence is a DNA encoding left chain of a heteromimibody
 CC comprising HD70 single-chain Fv (scFv) fragment N-terminally linked to
 CC human CH1 domain which bears at its C-terminus the human inflammatory
 CC cytokine granulocyte/macrophage colony stimulating factor (GM-CSF), plus
 CC a hexahistidine sequence for ease of purification. HD70 scFv
 CC specifically recognises the human epithelial cell adhesion molecule
 CC (EPCAM) also called 17-1A antigen.
 CC
 XX
 XX Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 other;
 SQ
 Query Match 48.5%; Score 445; DB 21; Length 1630;
 Best Local Similarity 76.3%; Pred. No. 1.3e-103;
 Matches 620; Conservative 0; Mismatches 145; Indels 48; Gaps 4

Db 576 CAGGCTCCAGGAGGGGCTGGAGTGGGCGAGTTATATCATATGAGTAATATA 635
 Oy 652 TACTACGACAGACTCCGTGAGAGGGCCGATTACCATCTCCAGAGACATTCCAAGAACG 711
 Db 636 TACTATGACAGACTCCGTGAGAGGGCCGATTACCATCTCCAGAGACATTCCAAGAACG 695
 Oy 712 CTGTATCTTAAAAATATAACGCTTGAGAACTGAGACACGGCTGTCTATTACTCTGCGAGA 771
 Db 696 CTGTATCTGCAAAATATAACGCTTGAGAGACACGGCTGTGTATTACTCTGCGAAA 755
 Oy 772 GATCAGACCTGTGGTGTACT-----ATGACCACTACTAGCGTTTGGACGCTGGGGC 825
 Db 756 GATATGGGGTGGGGGAGTGGCTGAGAGACCCCTACTACTACTACGATGAGACCTCTGGGAC 815
 Oy 826 AAGGGACACCGGTCAACCGCTCTCTCAGGATCC 858
 Db 816 CAAGGGACACCGGTCAACCGCTCTCTCCGGAAC 848
 RESULT 9
 AAD04530/C
 ID AAD04530 standard; DNA; 450 BP.
 AC AAD04530;
 XX
 DT 04-JUL-2001 (first entry)
 XX
 DE Human H11 antibody light chain variable region complementary DNA.
 XX
 KW Human; monoclonal antibody; Mab; H11; light chain variable region; scFv;
 KW single chain variable region; immunoglobulin IgM; gene therapy; lymphoma;
 KW neoplastic disease; melanoma; carcinoma; breast; lung; gastric; prostate;
 KW ovary; colon; lung; chronic leukaemia; neuroblastoma; vaccine; C-antigen;
 KW soft tissue sarcoma; cyrostatic; prostatic adenocarcinoma; glioma; de.
 XX
 OS Homo sapiens.
 XX
 FN US6207153-B1.
 XX
 PD 27-MAR-2001.
 XX
 PE 22-MAY-1997; 97US-0862124.
 PR 22-MAY-1996; 96US-0657449.
 PA (VIVE-) VIVENTIA BIOTECH INC.
 PI Dan MD, Maici PK, Kaplan HA;
 DR WPI; 2001-289584/30.
 PT Composition comprising antigen binding fragments of an antibody that
 PT recognize an antigen on neoplastic cells but not on normal cells for
 PT use in diagnosis, imaging and treatment of carcinomas
 PS Disclosure; Column 59-60; 56pp; English.
 XX
 XX The present sequence is human monoclonal antibody (Mab), H11 light chain
 CC variable region complementary DNA.
 CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)
 CC single chain variable (V) region fragment and their corresponding DNA
 CC molecules. H11 antibody is an immunoglobulin of IgM subclass which is
 CC specific to C-antigen found specifically on neoplastic cells and not on
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused
 CC to a human myeloma cell line to produce a hybridoma designated NBGM/H11.
 CC A pharmaceutical composition comprising H11 and its derivatives are
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,
 CC lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas
 CC and chronic leukaemias. H11 DNA is also used in vaccines and gene

CC therapy.
 XX
 SQ Sequence 450 BP; 105 A; 115 C; 134 G; 96 T; 0 other;
 Query Match 39.3%; Score 361; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. No. 2.4e-82;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 70 GATATTGTGTGACGACGATCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCA 129
 Db 378 GATATTGTGTGACGACGATCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAAGACCA 319
 Oy 130 CTCTCTCGAGGGCCAGTCAAGTGTATGTAGACACTTACTGCTGTACCAAGAAA 189
 Db 318 CTCTCTCGAGGGCCAGTCAAGTGTATGTAGACACTTACTGCTGTACCAAGAAA 259
 Oy 190 CCTGSCAGGGCTCCAGGCTCCTCATATGATGTGATCAACAGGGCCACTGGSCATGCCA 249
 Db 258 CCTGSCAGGGCTCCAGGCTCCTCATATGATGTGATCAACAGGGCCACTGGSCATGCCA 199
 Oy 250 GACAGGTTCAGTGAGTGGGTCCGGGACAGACTTCACTTCACCATCAGTAGACTGGAG 309
 Db 198 GACAGGTTCAGTGAGTGGGTCCGGGACAGACTTCACTTCACCATCAGTAGACTGGAG 139
 Oy 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAGTCACTTCAGACCTCAG 369
 Db 138 CCTGAAGATTTTGCAGTGTATTACTGTGACAGATATGTAGTCACTTCAGACCTCAG 79
 Oy 370 ATCACTTTCCGCGGAGGAGCCAAAGTGGAGATCAACGACTGTGGCTGCACCATCTGTC 429
 Db 78 ATCACTTTCCGCGGAGGAGCCAAAGTGGAGATCAACGACTGTGGCTGCACCATCTGTC 19
 Oy 430 T 430
 Db 18 T 18
 RESULT 10
 AAV10111
 ID AAV10111 standard; DNA; 450 BP.
 XX
 AC AAV10111;
 XX
 DT 29-MAY-1998 (first entry)
 XX
 DE Human monoclonal antibody H11 variable region H chain DNA.
 XX
 KW H11; monoclonal antibody; Mab; C-antigen; variable region heavy chain;
 KW V region; H chain; neoplasia; detection; lymphoma; tumour cell; probe;
 KW primer; vaccine; gene therapy; glioblastoma; neuroblastoma;
 KW malignant melanoma; adenocarcinoma; small cell lung carcinoma; ss.
 XX
 OS Homo sapiens.
 XX
 FN WO9744461-A2.
 XX
 PD 27-NOV-1997.
 XX
 PE 22-MAY-1997; 97WO-US08962.
 PR 22-MAY-1996; 96US-0657449.
 PA (NOVO-) NOVOPHARM BIOTECH INC.
 PI Dan MD, Kaplan HA, Maici PK;
 DR WPI; 1998-018515/02.
 DR P-PSDB; AAW40069.
 PT Antigen binding fragment from monoclonal antibody, H11 - allows
 PT tumour specific detection and treatment of neoplasia
 PS Claim 29; Page 87; 126pp; English.

XX This sequence encodes the human H11 monoclonal antibody variable (V)
 CC region heavy (H) chain which specifically recognises the C-antigen. Such
 CC an antigen binding fragment may be used for treating a patient with
 CC neoplasia. It is especially useful in the detection of lymphomas and
 CC leukaemias where the tumour cells bearing the C antigen are circulating
 CC in the patients bloodstream. The polynucleotide sequence may be used as a
 CC primer or a probe and the encoded protein may be used in a vaccine or
 CC for gene therapy. The human monoclonal antibody (Mab), designated H11,
 CC specifically recognises cancerous cells. H11 is specific for
 CC glioblastoma, neuroblastoma, malignant melanoma, breast adenocarcinoma,
 CC lung adenocarcinoma, small cell lung carcinoma, colon adenocarcinoma and
 CC prostate adenocarcinoma. The antigen binding fragment may also be used
 CC to detect C-antigen in a sample.

XX Sequence 450 BP; 96 A; 135 C; 115 G; 104 T; 0 other;

XX Query Match 39.2%; Score 359.4; DB 19; Length 450;

XX Best Local Similarity 99.7%; Pred. No. 6.2e-82; Indels 0; Gaps 0;

XX Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTTGACGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGCCACC 129

DB 73 GATATTGTGTTGACGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGCCACC 132

QY 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGTACGACTTACCTTGTAACCGACGAGAA 189

DB 133 CTCTCTGCGAGGGCCAGTCAAGTGTAGTACGACTTACCTTGTAACCGACGAGAA 192

QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACTGGCATGCCA 249

DB 193 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACTGGCATGCCA 252

QY 250 GACAGGTTGAGTGGGAGTGGGTCGGGACAGACTTCACTTCAACCATCAGTAACTGGAG 309

DB 253 GACAGGTTGAGTGGGAGTGGGTCGGGACAGACTTCACTTCAACCATCAGTAACTGGAG 312

QY 310 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTCACCTTCAGACACCTCAG 359

DB 313 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTCACCTTCAGACACCTCAG 372

QY 370 ATCACTTTGGGCGAGGACCAAGTGGAGATCAAGCACTGTGGCTGCACCATCTGTC 429

DB 373 ATCACTTTGGGCGAGGACCAAGTGGAGATCAAGCACTGTGGCTGCACCATCTGTC 432

QY 430 T 430

DB 433 T 433

RESULT 11

AAD04529 AAD04529 standard; DNA; 450 BP.

XX AAD04529;

XX 04-JUL-2001 (first entry)

XX Human monoclonal antibody (Mab), H11 light chain variable region DNA.

XX Human; monoclonal antibody; Mab; H11, light chain variable region; scFv;
 KW single chain variable region; immunoglobulin IGM; gene therapy; lymphoma;
 KW neoplastic disease; melanoma; carcinoma; breast; lung; gastric; prostate;
 KW ovary; colon; chronic leukaemia; neuroblastoma; vaccine; C-antigen;
 KW soft tissue sarcoma; cytostatic; prostatic adenocarcinoma; glioma; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 1..450

XX /product= "Human H11 light chain variable region"

XX /transl_except= (pos:259..261, aa:Phe)

FT /note= "CDS does not include start and stop codons"

FT /partial

PN US6207153-B1.

PD 27-MAR-2001.

PF 22-MAY-1997; 97US-0862124.

PR 22-MAY-1996; 96US-0657449.

PA (VIVE-) VIVENTIA BIOTECH INC.

PI Dan MD, Maiti PK, Kaplan HA;

DR WPI; 2001-289584/30.

DR P-PSDB; AAE00946.

PT Composition comprising antigen binding fragments of an antibody that
 PT recognizes an antigen on neoplastic cells but not on normal cells for
 PT use in diagnosis, imaging and treatment of carcinomas -

PS Disclosure; Column 57-58; 56pp; English.

XX The present DNA sequence encodes human monoclonal antibody (Mab), H11
 CC light chain variable region.

CC The invention relates to human monoclonal antibody (Mab) H11, H11-(scFv)
 CC single chain variable (V) region fragment and their corresponding DNA
 CC molecules. H11 antibody is an immunoglobulin of IGM subclass which is
 CC specific to C-antigen found specifically on neoplastic cells and not on
 CC normal cells. H11 is an antibody obtained from the fusion of peripheral
 CC blood lymphocytes of a 64 year old male with a low grade glioma and fused
 CC to a human myeloma cell line to produce a hybridoma designated NBGM/H11.

CC A pharmaceutical composition comprising H11 and its derivatives are
 CC useful in the diagnosis, imaging and treatment of neoplastic disease,
 CC particularly, melanoma, breast carcinoma, lung carcinoma, ovarian
 CC carcinoma, colon carcinoma, gastric carcinoma, prostate carcinoma,
 CC lymphoma carcinoma, neuroblastoma, glioma, soft tissue sarcoma, small
 CC cell lung carcinoma, prostatic adenocarcinoma, B and T cell lymphomas
 CC and chronic leukaemias. H11 DNA is also used in vaccines and gene
 CC therapy.

XX Sequence 450 BP; 96 A; 135 C; 115 G; 104 T; 0 other;

XX Query Match 39.2%; Score 359.4; DB 22; Length 450;

XX Best Local Similarity 99.7%; Pred. No. 6.2e-82; Indels 0; Gaps 0;

XX Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTTGACGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGCCACC 129

DB 73 GATATTGTGTTGACGAGTCTCCAGGACCCCTGCTTTGCTCCAGGGGAAAGCCACC 132

QY 130 CTCTCTGCGAGGGCCAGTCAAGTGTAGTACGACTTACCTTGTAACCGACGAGAA 189

DB 133 CTCTCTGCGAGGGCCAGTCAAGTGTAGTACGACTTACCTTGTAACCGACGAGAA 192

QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACTGGCATGCCA 249

DB 193 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACTGGCATGCCA 252

QY 250 GACAGGTTGAGTGGGAGTGGGTCGGGACAGACTTCACTTCAACCATCAGTAACTGGAG 309

DB 253 GACAGGTTGAGTGGGAGTGGGTCGGGACAGACTTCACTTCAACCATCAGTAACTGGAG 312

QY 310 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTCACCTTCAGACACCTCAG 359

DB 313 CTTGAAGATTTTTCAGTGTATTTACTGTACAGAGTATGTCACCTTCAGACACCTCAG 372

QY 370 ATCACTTTGGGCGAGGACCAAGTGGAGATCAAGCACTGTGGCTGCACCATCTGTC 429

DB 373 ATCACTTTGGGCGAGGACCAAGTGGAGATCAAGCACTGTGGCTGCACCATCTGTC 432

QY 430 T 430

PI Evans MD, Matis L, Mueller EE, Nye SH, Rollins S, Rother RP;
 PI Springhorn JP, Squinto SP, Thomas TC, Wang Y, Wilkins JA;
 DR WPI, 1995-392923/50.
 DR P-PSDB; AAR7617.
 PT Treating glomerulonephritis with antibody against complement C5
 PT component - to inhibit complement induced cell lysis
 XX
 PS Example 12; Page 147-149; 181pp; English.
 XX
 CC A DNA construct (AAR08490) codes for an anti-human complement
 CC C5 monoclonal antibody scFv (AAR7617). Unlike the native
 CC MAb, the scFv antibody was unable to block the generation of
 CC C5a and C5b-9 from C5. This was in contrast to a humanised
 CC scFv (see AAR7616) generated from MAb 5G1.1.
 CC (Updated on 25-MAR-2003 to correct PI field.)
 XX
 SQ Sequence 783 BP; 189 A; 195 C; 217 G; 182 T; 0 other;

Query Match 37.6%; Score 345.2; DB 16; Length 783;
 Best Local Similarity 69.3%; Pred. No. 36-78;
 Matches 552; Conservative 0; Mismatches 193; Indels 51; Gaps 4;

66 GGGCGATATTTGTTGACGAGTCTCCAGGACCCCTGTTCTTCAGGAGAAAGAGC 125
 3 GGGCATATTGTGTGACCAATCCATCTCAGCTTCTTGCTGTGTCTAGGAGAGGCG 62
 126 GACCTCTCTCTGACAGGGCCAGTCAGAGTGTAGTAG-----CAGTACTTATGCTTG 176
 63 CACCATATCTGACAGAGCCAGTGAAGTGTAGTATGACAAATGTTTATGACACTG 122
 177 GTACCGAGCAAAACCTGCGAGGCTCCAGGCTCCCATCTATATGAGCAATCCAGGAGC 236
 123 GTACCGAGCAAAACCTGCGAGGCTCCAGGCTCCCATCTATATGAGCAATCCAGGAGC 182
 237 CACTGCGATCCAGACAGGTTCCAGTGGGTCGGAGCCAGACTTCACTCTCAACAT 296
 183 ATCTGGGGTCCCTGCGAGGTTCCAGTGGGTCGGAGCCAGACTTCACTCTCAACAT 242
 297 CAGTGAAGTGGAGCTGGAAGTATTTGCAATGATTTACTGTGACAGTATGAGTCAACC 356
 243 TGATCTGTTGAGAGCTGATATGCTGCAACCTATTAATGTCAGCA-----AAA 290
 357 TCAGACACCTCAATATCTTCCGCGAGGAGCAAGAGTGAATCAAGAACTGTGGC 416
 291 TAATGAGTTCCGAACAGTTCCGAGGAGGAGCAAGAGTGAATCAAGAACTGTGGC 343
 417 TGCACCATCTGCTCTGCGAGGCTGTCGAGAGTGTGATCAAGTGAAGTGTGCTC 476
 344 -----CCGAGGTGGCGGGTGGGTTGGGCGGAGATCCGGTGGCGGAGGCTC 389
 477 CCAGGTGACGTGTGAGTCTTGGGGAGGCGGTGTCAGCTTGGAGGTCTCTGAGACT 536
 390 GAGAGTCAACCTGTGAGTCTGCGGAGAGCTTAAGTAACTTGGAGGTCCTGAAACT 449
 537 CTGCTGTGAGCTCTGAGTCTCCCTTCAAGAGTTTGTGATGACAGTGGTCCGCCAGC 596
 450 CTCTGTGAGCTCTGAGTCTTCACTTCAAGTGTATTAATGCTTGGGTTGGCGAGAT 509
 597 TCTAGGCAAGGGGCTGAGTGGTGGAGTATATCATATGATGAGAGCACTAAATCTA 656
 510 TTTCAGAGAAAGGCTGAGTGGTGGAGTATTAATGATGATGATGAGCACTTCTA 569
 657 CGCAGACTCTGTGAAGGGCGATTCACATCTCCAGAGACACTTCAAGAAACAGGTGTA 716
 570 TCCAGACACTGTGAAGGGCGATTCACATCTCCAGAGAAATGCCAAGAGCACCCTGA 629
 717 TCTAAATAATGAACGCTGAGAACTGAGAGACAGCGCTGTCTATATCTGTGCGAGATCA 776
 630 TCTGCAAAATGAGAGCTGTGAAGTCTGAGGACACAGCTTGTATTTCTGTGAAGAGA--- 666
 777 GAGCTGTGTGGTGAATATGACCACTACTAGGTTTGAAGTGTGAGGCAAGGAGCAAC 836

DB 687 -----GACTATTAATAAGGATTAATCCCTCTTCATGATGTTGGGACAGGACAC 740
 QY 837 GGTACACCTCTCTCTCA 852
 DB 741 GGTACACCTCTCTCTCA 756

RESULT 14
 ID AAT96346 standard; cDNA, 1848 BP.
 AC AAT96346;
 DT 08-APR-1998 (first entry)
 XX Chimeric gene containing anti-asparaginase MAb light and heavy chain.
 XX Immunoglobulin; Ig; heavy chain; variable region; murine; human;
 KM asparaginase II; monoclonal antibody; MAb; light chain;
 KM recombinant chimeric polypeptide; ss.
 OS Synthetic.
 OS Chimeric - Homo sapiens.
 OS Chimeric - Mus sp.
 PN US5686579-A.
 XX
 PD 11-NOV-1997.
 PD 23-MAY-1995; 95US-0447422.
 PF 22-JUN-1993; 93US-0081410.
 PR 21-JUN-1986; 88US-0205748.
 PR 31-AUG-1992; 92US-0938505.
 PR 23-MAY-1995; 95US-0447422.
 XX
 PA (HYBR-) HYBRISSENS LTD.
 PI Ramjessingh M, Rothstein A, Shani EY;
 DR WPI; 1997-558200/51.
 XX
 PT Self-protecting chimeric polypeptide comprising biologically active
 PT sequence and single-chain antibody sequence - has resistance to e.g.
 PT disrupting temperature, presence of proteolytic enzymes, etc.
 XX
 PS Example 2; Columns 27-30; 29pp; English.
 XX
 CC The present sequence is a chimeric gene containing the cDNA for
 CC the immunoglobulin (Ig) heavy and light chain variable regions of a
 CC murine anti-asparaginase II monoclonal antibody (MAb), and human
 CC asparaginase II. The gene was used in the preparation of a novel
 CC recombinant chimeric polypeptide, comprising a 1st region
 CC comprising a biologically active domain and another domain
 CC containing an epitope, linked via a polypeptide to a 2nd region
 CC including a single chain antibody (SCA) having the light and heavy
 CC chains of an antibody variable region which specifically binds the
 CC epitope in the 1st region. The chimeric polypeptide assumes a
 CC conformation in which the SCA is bound to the epitope of the 1st
 CC region and protects its biological activity from deactivation by
 CC denaturing temperatures or pH conditions, proteolytic enzymes,
 CC oxidising agents or alcohol. The regions of the chimeric
 CC polypeptide interact to form a structure analogous to an
 CC antibody-antigen complex. A D-asparaginase-SCA fusion protein of
 CC the above type has better trypsin resistance than free
 CC L-asparaginase.
 XX
 SQ Sequence 1848 BP; 435 A; 498 C; 517 G; 398 T; 0 other;

Query Match 37.4%; Score 343.6; DB 18; Length 1848;
 Best Local Similarity 72.3%; Pred. No. 9,4e-78;
 Matches 483; Conservative 0; Mismatches 164; Indels 21; Gaps 2;

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QY 70 GATATTTGTTGACGAGTCTTCAGGACCTGTCTTTGTCTTCAGGGGAAAGACCAC 129
DB 1 GATATTTGTTGACGAGTCTTCAGGACCTGTCTTTGTCTTCAGGGGAAAGACCAC 60
QY 130 CTCTCTGACGGGCGAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 189
DB 61 ATGACCTGACGGGCGAGTGTATGATGATGATGATGATGATGATGATGATGATGAT 120
QY 190 CTGAGGCGAGTCTTCATCTATGATGATGATGATGATGATGATGATGATGATGAT 249
DB 121 TCAGTGTCTCTCCCAAGTCTGATTTATGACATCTCAATCTGCTTCTGATCTCT 180
QY 250 GACAGTTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 309
DB 181 GCTGCTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 240
QY 310 CCTGAAATTTTGTGAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 369
DB 241 GCTGAAATGCTGTGACCTTATGATGATGATGATGATGATGATGATGATGATGAT 289
QY 370 ATCACTTTCGAGGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 427
DB 290 -TCAGCTTCGAGGCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 348
QY 428 -----TCTGTGCGGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 480
DB 349 TCCATCTTCGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 408
QY 481 GTGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 540
DB 409 GTCAAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 468
QY 541 TGTGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 600
DB 469 TGTGAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAG 528
QY 601 GCGAAGGGGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 660
DB 529 GAGAAAGGGGCGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 588
QY 661 GACTCCGTTGAGGCGGATTCATCTTCAGAGACATTCCTCAAGAACCGGTGATCTA 720
DB 589 GACACAGTGTGAGGCGGATTCATCTTCAGAGACATTCCTCAAGAACCGGTGATCTA 648
QY 721 AAAATGAA 728
DB 649 CAATGAA 656

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RESULT 15
AAT79537
ID AAT79537 standard; DNA; 5227 BP.

AAT79537;
06-MAR-1998 (first entry)
Plasmid pTERMEC2H10myc38CM.
Protein-protein interaction; interacting polypeptide;
polyphage principle; plasmid pTERMEC2H10myc38CM; vector;
Escherichia coli display; peptide library; ds.
Synthetic.
W09732017-A1.
04-SEP-1997.
26-FEB-1997, 97MO-BP00931.
26-FEB-1996, 96EP-0102852.

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XX (MORP-) MORPHOSYS GES PROTEINOPTIMIERUNG MBH.
PA Ge L, 1lag V.
PI WPI, 1997-448687/41.
XX
XX Identification of interacting polypeptide encoding nucleic acid
PT sequences - e.g. to identify protein-protein interactions, which
PT play an important role in biological processes
PS Example 8, Fig 25; 105pb; English.
XX
XX Plasmid pTERMEC2H10myc38CM (AAT79537) can be used in a novel method
CC for identifying nucleic acid sequences (NAS), which encode
CC polypeptides capable of interacting with at least 1 of their fellow
CC polypeptides. This comprises: (a) providing a 1st library of
CC recombinant vectors containing genetically diverse NAS comprising a
CC variety of NAS encoding polypeptides; (b) providing a 2nd library of
CC recombinant vectors containing genetically diverse NAS comprising a
CC variety of NAS encoding polypeptides capable of interacting with
CC the polypeptides of (a), where the vectors employed for production
CC of the recombinant vectors and/or recombinant inserts display
CC properties that are phenotypically distinguishable from those used
CC in (a), and where at least 1 of the properties displayed by the
CC vectors and/or recombinant inserts used in steps (a) and (b), upon
CC the interaction of a polypeptide from the 1st library with a
CC polypeptide from the 2nd library, together generate a screenable or
CC selectable property; (c) expressing members of the libraries of
CC recombinant vectors or nucleic acid sequences of (a) and (b), in
CC appropriate host cells so that at least 1 interaction is
CC established; and (d) selecting for the generation of the
CC screenable or selectable property representing the interaction of
CC the polypeptides. The method can be used to identify protein-protein
CC interactions.
SQ Sequence 5227 BP; 1232 A; 1265 C; 1355 G; 1375 T; 0 other;
Query Match 35.7%; Score 328; DB 18; Length 5227;
Best Local Similarity 65.7%; Pred. No. 1,2e-73;
Matches 594; Conservative 0; Mismatches 235; Indels 75; Gaps 5;
QY 2 AATTCATGAAAAAACCCTATGCGATGCGAGTTGACACTGCGTGTGCTTACCGTTG 61
DB 1378 AAAAAATGAAAAAGACAGCTATCGGATTCAGTGGCACTGGCTGTTTCGTTACCGTTG 1437
QY 62 CGCAGGCC-----GATATTTGTTGAGCGAGTCTTCAGGACACCTGTCTTGTCTTC 112
DB 1438 CGCAGGCCGACTACAAAGATATCGATGATGACCAAGTCTTCAGCAATCATGCTTACATCTC 1497
QY 113 CAGGGGAAAGAGCCACCTCTCTGACAGGCGCAGTCAAGTGTGATGACGACTTAG 172
DB 1498 TTAGGGAACGGGTCACTATGACTGCTGCTGCTTCAAGTGAATGCTCTTACTTAC 1557
QY 173 CTTGTATCAGCAGAAACCTGCGCAGGCTCCAGGCTCTCTCATCTATGATGATCCACCA 232
DB 1558 ACTGTATCAGCAGAAAGCAGGATCTCCCAAACTGTGATTTATGACATCAAC 1617
QY 233 GGGCAGCTGCGATGCGACAGTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 292
DB 1618 TGGCTTCTGAGTCTCCCACTGCTTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1677
QY 293 CCATGATGATGATGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 352
DB 1678 CATGATGATGATGAGGCTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1737
QY 353 CACTTCAGACACTGATGATCTTTGCGCGAGGAGCAAGAGTGTGATGATCAAAAGCACTG 412
DB 1738 TCCGAC-----CAAGCTTCGAGGGGGAGCAAGAGTGTGATGATGATGATGATGATG 1780
QY 413 TGGCTGACCATCTCTCTGCGCGGTGCGGAGTGTGATGATGATGATGATGATGATGATG 472
DB 1781 -----GGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1824

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QY 473 GCTCCAGGTGCACTGTGTGAGTCTGGGGAGGCGTGTCCAGCCTGGAGGTCCTGA 532
Db 1825 GTTCTGAAGTTAACTGTGAGTCTGGAGAGGCTTGTGCACTGGAGATCCATGA 1884
QY 533 GACTTCCTGTGAGGCTCTGATCCCTTCAGAACTTGTCTATGCACTGGGTCGCC 592
Db 1885 AACTTCCTGTGTGCTTCTGGAATCACTTCAGTAATTACCGGATGAACCTGGGTCGCC 1944
QY 593 AGGCTCTAGGCAAGGGGCTGAGTGGGTGGCAGTTA-----TATCATATGATGAAGCA 646
Db 1945 AGTCTCAAGAGAAAGGGGCTTGAAGGTTGCTGAATTAATTGAATTAATTAATTAATG 2004
QY 647 CTAAATTAAGCAAGTCCGTGAAGGCGGATTCACCATCTCCAGAGACACTTCCAGA 706
Db 2005 CAACACATTAATGGAGTCTGTGAAAGGAGGTTCAACATCTCAAGAGATGATTCAGAAA 2064
QY 707 ACAGGGTGTATCTAAAAATGAAACAGCCTGAGAACTGAGACACGGTGTCTATTACTGTG 766
Db 2065 GTTAGTGTCTACTGCAAAATGAACAACTTAAGAGCTGAAGACACTGGCATTTATTACTGTA 2124
QY 767 CGAGAGATCAGAGGCTGTGGGTGACTATGACCACTACTACGGTTGGACGTCTGGGCA 826
Db 2125 GAGGGGTT-----TCATATACTATAGACTAGGGGTC 2157
QY 827 AAGGGACCAAGGTCAACCGTCTCTCTCAGGATCCGAACAAACTGATCAGGAGAAAGATC 886
Db 2158 AAGGAACCTCAGTCACAGTCTCTCTCAGAAATTCAGAGAACTGATCTGTAGAGAAAGCC 2217
QY 887 TGA 890
Db 2218 TGT 2221
```

Search completed: September 17, 2003, 03:07:12
Job time : 261 secs

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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 02:58:44 ; Search time 63 Seconds

(without alignments)
6431.583 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgn2_6/prodata/2/1na/5A_COMB.seq: *
2: /cgn2_6/prodata/2/1na/5B_COMB.seq: *
3: /cgn2_6/prodata/2/1na/6A_COMB.seq: *
4: /cgn2_6/prodata/2/1na/6B_COMB.seq: *
5: /cgn2_6/prodata/2/1na/PCTUS_COMB.seq: *
6: /cgn2_6/prodata/2/1na/Backfillseq1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	3	US-08-862-124-13 Sequence 13, Appl
2	916.4	99.8	918	3	US-08-862-124-15 Sequence 15, Appl
3	799.6	87.1	867	3	US-08-862-124-16 Sequence 16, Appl
4	798	86.9	867	3	US-08-862-124-18 Sequence 18, Appl
5	361	39.3	450	3	US-08-862-124-6 Sequence 6, Appl
6	359.4	39.2	450	3	US-08-862-124-4 Sequence 4, Appl
7	345.2	37.6	783	4	US-08-487-283A-19 Sequence 19, Appl
8	343.6	37.4	1848	1	US-08-447-422-15 Sequence 15, Appl
9	324.4	35.3	543	3	US-08-862-124-3 Sequence 3, Appl
10	324.4	35.3	543	3	US-08-862-124-1 Sequence 1, Appl
11	318.4	34.7	4691	4	US-08-591-632-43 Sequence 43, Appl
12	318.4	34.7	4691	4	US-08-611-451-43 Sequence 51, Appl
13	318.4	34.7	6166	3	US-08-591-632-51 Sequence 51, Appl
14	318.4	34.7	6166	4	US-09-611-451-51 Sequence 51, Appl
15	303.6	33.1	1797	4	US-08-442-542-17 Sequence 17, Appl
16	303.6	33.1	1797	3	US-08-765-469-17 Sequence 17, Appl
17	300.6	32.7	752	6	5455030-12 Patent No. 5455030
18	289.4	31.5	402	1	US-08-405-034-3 Sequence 3, Appl
19	287.4	31.3	378	1	US-09-240-274-95 Sequence 95, Appl
20	287.2	31.3	723	1	US-07-988-430-92 Sequence 92, Appl
21	287.2	31.3	723	1	US-08-425-336-89 Sequence 89, Appl
22	287.2	31.3	723	1	US-08-488-113B-89 Sequence 89, Appl
23	287.2	31.3	723	1	US-08-477-484B-89 Sequence 89, Appl
24	287.2	31.3	723	2	US-08-646-360-89 Sequence 89, Appl
25	287.2	31.3	723	3	US-08-839-765-89 Sequence 89, Appl
26	287.2	31.3	723	3	US-09-136-389-89 Sequence 89, Appl
27	287.2	31.3	723	4	US-09-610-838-89 Sequence 89, Appl

28	287.2	31.3	723	5	PCT-US92-09487-92 Sequence 92, Appl
29	286	31.2	375	3	US-09-240-274-194 Sequence 194, Appl
30	284.2	31.0	378	3	US-09-240-274-94 Sequence 94, Appl
31	284.2	31.0	378	3	US-09-240-274-196 Sequence 196, Appl
32	283.8	30.9	784	2	US-08-956-047-32 Sequence 32, Appl
33	282.2	30.7	741	6	5455030-10 Patent No. 5455030
34	282	30.7	733	2	US-08-824-591-17 Sequence 17, Appl
35	281.2	30.6	900	1	US-08-926-789-17 Sequence 182, Appl
36	281.2	30.6	900	1	US-08-053-131-182 Sequence 182, Appl
37	281.2	30.6	900	3	US-08-096-762-182 Sequence 182, Appl
38	281.2	30.6	900	3	US-09-042-353-45 Sequence 45, Appl
39	281.2	30.6	900	4	US-08-758-417A-310 Sequence 310, Appl
40	281	30.6	369	4	US-09-560-178A-1 Sequence 1, Appl
41	281	30.6	378	3	US-09-240-274-195 Sequence 195, Appl
42	280.6	30.6	645	2	US-08-480-753-7 Sequence 7, Appl
43	278.2	30.3	646	1	US-08-300-386A-2 Sequence 2, Appl
44	278.2	30.3	646	3	US-08-931-645-2 Sequence 2, Appl
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ALIGNMENTS

RESULT 1
US-08-862-124-13
; Sequence 13, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maitl, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
; TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; TITLE OF INVENTION: DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/862,124
; FILING DATE: 22-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..906, 913..918)
US-08-862-124-13
Query Match 100.0%; Score 918; DB 3; Length 918;
Best Local Similarity 100.0%; Pred. No. 9,8e-252;

Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCGCAGGCGGATATTTGGTTGACGACATCTCCAGGCAACCGTCTTGTCTCCAGGGGAA 120
DB 61 GCGCAGGCGGATATTTGGTTGACGACATCTCCAGGCAACCGTCTTGTCTCCAGGGGAA 120

QY 121 AGAGCCACCTCTCTGCGACAGGCGCAGTCAAGTGTATGATGACAGCTACTTACGCTGTGAC 180
DB 121 AGAGCCACCTCTCTCTGCGACAGGCGCAGTCAAGTGTATGATGACAGCTACTTACGCTGTGAC 180

QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 240
DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 240

QY 241 GGCATGCGACAGGTTCAGTGCGAGTGGGTCGCGGACAGACTTCACTCTCACCACAT 300
DB 241 GGCATGCGACAGGTTCAGTGCGAGTGGGTCGCGGACAGACTTCACTCTCACCACAT 300

QY 301 AGACTGAGCCTGAGATTTTGCAGTGTATTAATGTCAGAGATATGATGCTCACTCAG 360
DB 301 AGACTGAGCCTGAGATTTTGCAGTGTATTAATGTCAGAGATATGATGCTCACTCAG 360

QY 361 ACACCTCAGATCACTTTGCGCGAGGAGGACCAAGGTGAGATCAAAACGAACTGTGCTGCA 420
DB 361 ACACCTCAGATCACTTTGCGCGAGGAGGACCAAGGTGAGATCAAAACGAACTGTGCTGCA 420

QY 421 CCATCTGCTCTGCGGCGGTCGCGGAGTGTGATGATGATGATGATGATGATGATGATGAT 480
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DB 481 GTGCAAGTGTGAGTGTGCGGAGGAGGCGTGTGATGATGATGATGATGATGATGATGAT 540

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DB 541 TGTGCAAGTGTGATTTCCCTTCAAGAGCTTTGCTATGATGATGATGATGATGATGATGAT 600

QY 601 GCGCAAGGCGGCTGAGTGGTGGAGTATATCATATGATGATGATGATGATGATGATGATGAT 660
DB 601 GCGCAAGGCGGCTGAGTGGTGGAGTATATCATATGATGATGATGATGATGATGATGATGAT 660

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DB 661 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGCACTTCCAGAGCAACGCTGTATCTA 720

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QY 901 CACCATTAAGTAAAGCTT 918
DB 901 CACCATTAAGTAAAGCTT 918

RESULT 2
US-08-657-449-13/c
Sequence 15, Application US/0862124
Patent No. 6207153
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.

APPLICANT: Maiti, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-657-449-13

Query Match 99.8%; Score 916.4; DB 3; Length 918;
Best Local Similarity 99.9%; Pred. No. 2.8e-251;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCGCTATGCGATGCGATGCGATGCGTGGTTTCCGTAACGTT 60
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QY 121 AGAGCCACCTCTCTGCGACAGGCGCAGTCAAGTGTATGATGACAGCTACTTACGCTGTGAC 180
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QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 240
DB 738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGCTGATCACCAGGGCCACT 679

QY 241 GGCATGCGACAGGTTCAGTGCGAGTGGGTCGCGGACAGACTTCACTCTCACCACAT 300
DB 678 GGCATGCGACAGGTTCAGTGCGAGTGGGTCGCGGACAGACTTCACTCTCACCACAT 619

QY 301 AGACTGAGCCTGAGATTTTGCAGTGTATTAATGTCAGAGATATGATGCTCACTCAG 360
DB 618 AGACTGAGCCTGAGATTTTGCAGTGTATTAATGTCAGAGATATGATGCTCACTCAG 559

QY 361 ACACCTCAGATCACTTTGCGCGAGGAGGACCAAGGTGAGATCAAAACGAACTGTGCTGCA 420
DB 558 ACACCTCAGATCACTTTGCGCGAGGAGGACCAAGGTGAGATCAAAACGAACTGTGCTGCA 499

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Db	498	CCATCTGTCCTGAGCGGTGCGGTTCCGAGGCGTGGATCAGGTGGAGTGGCTCCAC	439
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Db	438	GTCGACGTGTGTGGAGTCTTGGGGGAGGGCGTGTCCAGCTTGGGAGGTCCCTGAGACTCTCC	379
Qy	541	TGTGACGCTCTGSAATCCCTTCAGAACTTGTGATGCACTGGGTCCGCCAGGCTCTA	600
Db	378	TGTGACGCTCTGSAATCCCTTCAGAACTTGTGATGCACTGGGTCCGCCAGGCTCTA	319
Qy	601	GGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCACTAAATCTACGCA	660
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Qy	841	ACCGTCTCTCAAGATCCGAAACAAAACTGATCAGGGAAGAGATCGAACCTACACAT	900
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?      SEQUENCE CHARACTERISTICS:
?      LENGTH: 867 base pairs
?      TYPE: nucleic acid
?      STRANDEDNESS: single
?      TOPOLOGY: linear
?
?      FEATURE:
?      NAME/KEY: CDS
?      LOCATION: join(1..855, 862..867)
?
?      US-08-862-124-16

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APPLICANT: Thomas, Thomas C.
 APPLICANT: Wilkins, James A.
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT
 TITLE OF INVENTION: OF INFLAMMATORY DISEASES
 NUMBER OF SEQUENCES: 26
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seth A. Fidel
 STREET: 25 Science Park (Alexion)
 CITY: New Haven
 STATE: Connecticut
 COUNTRY: USA
 ZIP: 06511
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.4mb storage
 COMPUTER: Macintosh Cetrus 610
 OPERATING SYSTEM: System 7
 SOFTWARE: WordPerfect 3.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/487,283A
 FILING DATE: June 7, 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/236,208
 FILING DATE: 02-MAY-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Seth A. Fidel
 REGISTRATION NUMBER: 38,449
 REFERENCE/DOCKET NUMBER: ALX-152.1 CIP
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (203) 776-1790
 TELEFAX: (203) 772-3655
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 783 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: Double
 TOPOLOGY: linear
 MOLECULE TYPE: Other nucleic acid
 DESCRIPTION: N19/8 scFv (His Tagged)
 US-08-487-283A-19

Query Match 37.6%; Score 345.2; DB 4; Length 783;
 Best Local Similarity 69.3%; Pred. No. 9.5e-89;
 Matches 552; Conservative 0; Mismatches 193; Indels 51; Gaps 4;

QY 66 GGGGATATTTGTGTTGACGAGTCTCCAGSCACCCTGTTGTTCTCCAGGGGAAAAGC 125
 DB 3 GGGCAATATTTGTGTTGACCCCAATCTCCAGCTTCTTGTGCTGTCTAGGGGCAAGGCG 62
 QY 126 CACCTCTCTGCGAGGGGCGAGTCTAGAGTTAGTAG-----CAGCTACTAGGCTG 176
 DB 63 CACCATATCTGCGAGGCGAGTGAAGTGTGATGATTATGACAAATGTTTATGCACTG 122
 QY 177 GTACAGAGAAACCTGCGAGGCTCCAGGCTCTCATCTATGATGATCCACAGGCG 236
 DB 123 GTACAGAGAGAAACAGAGAGAGCAACCAACTCTCTATCTTTCTGATCAACCTAGA 182
 QY 237 CATTGGATGCCAGAGAGTTCAGTGGAGTGGGTCGGGAGCAAGTCTTCACTTCACCAT 296
 DB 183 ATCTGGGGTCTCTCCAGGTTCAAGTGGGAGTGGGCTCTAGGAGCAAGCTTCAACCTCACCAT 242
 QY 297 CAGTAGAGTGAAGCTGAAGTTTTCAGTGTATTACTGAGAGAGTAGTAGTCAACC 356
 DB 243 TGATCTGTGAGGCTGATGATGCTGCAACTATTACTGTACAG-----AAA 290
 QY 357 TCAGACACTCAGATCACTTTTCGGCGAGGAGCAAGGTGAGATCAAAAGCACTGTGGC 416
 DB 291 TAAATGAGGTTCGAACAGTTCGGAGGGGGAGCAAGCTGGAATAAAGCA----- 343
 QY 417 TGACCATCTGTCTGTGGCGGTGGGGTTCGGAGAGTGTGATCAGGTGAGGTGGCTC 476
 DB 344 -----CCGAGGTGGGGGTGGGGTGGGGTGGGGGAGTGGGGTGGGGAGGGTTC 389
 QY 477 CCAAGTGAAGTGTGAGTGTGGGGGAGGGGTGTGTCAGGCTGGGAGGTCCCTGAGACT 536

DB 390 GGACGTCAAGCTGTGAGACTCTGGGGAGACTAGTAAGCTTGAGGGGTCTCCCTGAACT 449
 QY 537 CTCTGTGACGCTCTGATTCCTCCCTTCGAAGCTTGTCTATGACACTGGGTCCGCCAGGC 596
 DB 450 CTCTGTGACGCTCTGATTCCTCCCTTCGAAGCTTGTCTATGACACTGGGTCCGCCAGGC 509
 QY 597 TCTAGGCAAGGGGCTGAGTGGGGTGGGCACTTATATCATATGATGAGCACTAAATACTA 656
 DB 510 TTCAGAGAAAGAGCTGAGTGTGTGCGACCCATTATATGATGATGATGATGATGATGAT 569
 QY 657 CGCAGACTCCGTGAAGGGCCGATTCACATCTCCAGAGACACTTCCAGAAACCGGTGA 716
 DB 570 TCCAGACACTGTGAAGGGCCGATTCACATCTCCAGAGCAATGCAAGAGCACTCTGA 629
 QY 717 TCTAAATGAACGCTGAGAACTGAGAGACAGGCTGTCTATGATGATGATGATGATGAT 776
 DB 630 TCTGCAAAATGAGAGCTGAGTGTGAGAGACAGGCTGTGTATTTCTGTGTAAAGA--- 686
 QY 777 GAGCTGTGGGTAAGTATGACCACTAGAGGTTGAGAGTCTGGGGCAAGGAGCCAC 836
 DB 687 -----GACTTATTACTAGGGATTAATGCTCCCTTCGATGTCTGGGGCAAGGAGCCAC 740
 QY 837 GGTACCGTCTCCTCA 852
 DB 741 GGTACCGTCTCCTCA 756

RESULT 8
 US-08-447-422-15
 Sequence 15, Application US/08447422
 Patent No. 5686579
 GENERAL INFORMATION:
 APPLICANT: SHAMI, Ezekiel Y.
 APPLICANT: ROTHSTEIN, Aseer
 APPLICANT: RAMJESINGH, Monabit
 TITLE OF INVENTION: Use of Antibody/Antigen Interactions To
 TITLE OF INVENTION: Protect or Modulate Biological Activity
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Foley & Lardner
 STREET: 3000 K Street, N.W., Suite 500
 CITY: Washington, D.C.
 COUNTRY: USA
 ZIP: 20007-5109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/447,422
 FILING DATE:
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/081,410
 FILING DATE: 22-JUN-1993
 APPLICATION NUMBER: US 07/938,505
 FILING DATE: 31-AUG-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/205,748
 FILING DATE: 21-JUN-1988
 ATTORNEY/AGENT INFORMATION:
 NAME: BENT, Stephen A.
 REGISTRATION NUMBER: 29,768
 REFERENCE/DOCKET NUMBER: 17923/102 HYLI
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 672-5300
 TELEFAX: (202) 672-5399
 TELEX: 904136
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1848 base pairs


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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-447-422-15

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Query Match	37.4%;	Score 343.6;	DB 1;	Length 1848;
Best Local Similarity	72.3%;	Pred. No. 3.9e-88;		
Matches 483; Conservative	0;	Mismatches 164;	Indels 21;	Gaps 2

Oy 70 CATATTTGTTGACCCAGGCTCTCAGGACACCCGTCCTTTGCTTCACAGGGGAAAGAGCAC 129
 Db 1 GATATTTGCTCTCACTCAATCCGACGATCATGTCTGCATCTTCACAGGGGAAAGGTCACC 60
 Oy 130 CTCTCTCTCAAGGCGCAGTCAGAGTGTATTAGACAGTACTTAAGCCTGTATCCAGCAGAAA 189
 Db 61 ATGACCTCTCAAGGCGCAGCTCAAGTGAAGTTACAGTTACTTGACCTGTATCCAGCAGAAAG 120
 Oy 190 CTTGGCCACAGGCTCCCAAGGCTCTCATATATGTGTGATCCACCAAGGCGCACTGGCATGCCA 249
 Db 121 TCAGGTGCTCTCCCAAACTCTGGAATTTATACACATCCAACTTGGCTTCTTGAGTCCCT 180
 Oy 250 GACAGGTTCAAGTGGAGTGGGTCCGGGACAGACTTCACTCTACCATTCAGTATGACCTGGAG 309
 Db 181 GCTGCTTCAAGTGGAGTGGGTCTGGGACTCTTACTCTCTCAATTCAGCAGTGTGGAG 240
 Oy 310 CCTGAGAGATTTTGCAGTGTATTACTGTGCAGAGTATGTAGTACCTCAAGACCTCAG 369
 Db 241 GCTGAGAGTCTGCGCACTTATTACTGCCAGCAGTACAGTGTATCCAC----- 289
 Oy 370 ATCATTTTCGGCGAGGAGCCAAAGGTGAGATCAACGAACTGTGGCTGCACCATCTG-- 427
 Db 290 -TCACGTTCCGAGGGGGGAGCCAAAGCTGGAAATATAAACGGGCTGATGCTGCACCAACTGTA 348
 Oy 428 -----TCTCTGCGGTGTGGCGGCTTCGGAGGTGTGTGATCAAGTGTGAGGTGGCTCCAG 480
 Db 349 TCCATCTTCCAGGTGGGTGGCTTCGGCGGTGGGTGGGTGGGTGGGTGGGTGGGTGGGTGG 408
 Oy 481 GTGACGCTGTGTGATCTGTGGGAGGCGGTGTGCAAGCTCGGAGAGTCCCTGAGACTCTCC 540
 Db 409 GTCAAGCTGCAGAGAGTCTGGGGGAGGCTTAGTGCAGCTCGAGAGGTCCCGGAAACTCTCC 468
 Oy 541 TGTGAGGCTCTGGAATCTCCCTTCAGAAAGCTTTGCTATGACACTGGGTCCGACAGGCTCTA 600
 Db 469 TGTGAGGCTCTGGAATCTCTTCACTTCACTGAGTCTTTGGAATGACACTGGGTGTGTGAGCTCA 528
 Oy 601 GGCAAGGGGCTGTGAGTGGGTGGTGCAGTTATATATATGATGAGAAACACTAAATATCAAGCA 660
 Db 529 GAGAAAGGGGCTGTGAGTGGGTGGTGCATATATATGATGAGTGGTGGTGGTGGTGGTGGTGG 588
 Oy 661 GACTTCGTGAAAGGCGCGATTCACCATCTTCAGAGACACTTCAGAAACAGGCTGATCTTA 720
 Db 589 GACACAGTGAAGGGCGGATTCACCATCTTCAGAGACAAATCCAGAAACACCTGTCTCTG 648
 Oy 721 AAAATGAA 728
 Db 649 CAAATGAA 656
 RESULT 9
 US-08-862-124-1
 Sequence 1, Application US/08862124
 Patent No. 6207153
 GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 APPLICANT: Maif, Pradip K.
 APPLICANT: Kaplan, Howard A.
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
 SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
 FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
 TREATMENT OF CANCERS
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESS: Motrilson & Foerster LLP

```

STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/862,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..543
US-08-862-124-1

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Query Match	35.3%	Score 324.4;	DB 3;	Length 543;
Best Local Similarity	89.3%;	Pred. No. 6.7e-83;		
Matches 349;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;

[illegible]

RESULT 10
US-08-862-124-3/c
; Sequence 3, Application US/08862124
; Patent No. 6207153
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.

APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,124
FILING DATE: 22-MAY-1997
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 543 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-662-124-3

Query Match 35.3%; Score 324.4; DB 3; Length 543;
Best Local Similarity 89.3%; Pred. No. 6,7e-83;
Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 440 GCGGTCCGAGGTGTGATCAGGTGAGGTGCTCCAGGTGAGGTGAGTCTG 499
Db 392 GGGTTCCTCTGCTCTTTTAAGAGTATCCAGTGTGAGTGTGAGTCTG 333
QY 500 GGGGAGCGTGTGTCAGCTGAGGTGAGTCTGAGTCTCTCTGTGAGCCTCTGATTC 559
Db 332 GGGGAGCGTGTGTCAGCTGAGGTGAGTCTCTGAGTCTCTCTGTGAGCCTCTGATTC 273
QY 560 CCTTCAGAGTGTGCTATGATCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 619
Db 272 CTTTCAAGCTTGTGATGATGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 213
QY 620 TGGCAGTATATCATATGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 679
Db 212 TGGCAGTATATCATATGATGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTGAGTCTG 153
QY 680 TCACCATCTCCAGAGACATCTTCAAGAACAGAGTGTATCTTAAATGAAACAGCTGAGAA 739
Db 152 TCACCATCTCCAGAGACATCTTCAAGAACAGAGTGTATCTTAAATGAAACAGCTGAGAA 93
QY 740 CTGAGGACAGGCTGTCTATTAATCTGTGAGAGATCAAGGCTGTGAGTGTATGATGAC 799
Db 92 CTGAGGACAGGCTGTCTATTAATCTGTGAGAGATCAAGGCTGTGAGTGTATGATGAC 33
QY 800 ACTACTAGCGTTTGAAGCTCTGAGGCAAGG 830
Db 32 ACTACTAGCGTTTGAAGCTCTGAGGCAAGG 2

RESULT 11
US-08-591-632-43

Sequence 43, Application US/08591632
Patent No. 6261558
GENERAL INFORMATION:
APPLICANT: Barbac, Carlos F.
APPLICANT: Burton, Dennis R.
APPLICANT: Lerner, Richard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
TITLE OF INVENTION: ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
ADDRESSEE: Patent Counsel
STREET: 10550 No. 6261558th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,632
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/11907
FILING DATE: 19-OCT-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 4691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-591-632-43
Query Match 34.7%; Score 318.4; DB 3; Length 4691;
Best Local Similarity 88.4%; Pred. No. 8,7e-81;
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;
QY 7 ATGAAAAAAGCCCTTATCCGATGCAAGTTCAGTCTGCTGCTACCTGTTGGCAG 66
Db 2611 ATGAAAAAAGCCCTTATCCGATGCAAGTTCAGTCTGCTGCTACCTGTTGGCAG 2670
QY 67 GCGGATATGTGTGAGGAGTCTCCAGGACCTGTCTTGTCTCAGGGGAAAGGCC 126
Db 2671 GCGG---CCGAGTCTCAGGAGTCTCCAGGACCTGTCTTGTCTCAGGGGAAAGGCC 2727
QY 127 ACCCTCTCTGCAAGGCGCAGTCAAGTGTAGTACAGTACTTACCTGTGTACAGAG 186
Db 2728 ACCCTCTCTGCAAGGCGCAGTCAAGTGTAGTACAGGCGCTACTTACCTGTGTACAGAG 2787
QY 187 AAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCATGCGCATG 246
Db 2788 AAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGCGCATGCGCATG 2847

ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
US-08-591-632-51

Query Match 34.7%; Score 318.4; DB 3; Length 6166;
Best Local Similarity 88.4%; Pred. No. 9.7e-81;
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY 7 ATGAAAAAACCGCTATGCGGATCGCATGTCAGTGGCTGGTTCCTACCGTTGCCGAG 66
DB 4541 ATGAAAAAGACAGCTATGCGATTCAGTGGCAGTGGCTGGTTCCTACCGTTGCCGAG 4600
QY 67 GCCGATATTTGTTGACGAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAAAGAGCC 126
DB 4601 GCGG---CCGAGCTCAGCGAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAAAGAGCC 4657
QY 127 ACCCTCTCTCGAGGGGCGAGTCAAGTGTAGTACAGCTTACCTTGTGTTACCAAGAG 186
DB 4658 ACCCTCTCTCGAGGGGCGAGTCAAGTGTAGTACAGGGGCTTACCTTGTGTTACCAAGAG 4717
QY 187 AAACCTGGCCAGGCTCCAGAGGCTCTCATCTATGTTGATCCACAGGGGCACTGGCAGT 246
DB 4718 AAACCTGGCCAGGCTCCAGAGGCTCTCATCTATGTTGATCCACAGGGGCACTGGCAGT 4777
QY 247 CCAGACAGGTTCAGTGGAGTGGTCCGGGACAGACTTCACTCTCACCATCAGTAGACTG 306
DB 4778 CCAGACAGGTTCAGTGGAGTGGTCTGGGACAGACTTCACTCTCACCATCAGTAGACTG 4837
QY 307 GAGCTGGAAGATTTTGCAGTGTATCTGTACAGCACTATGTTAGTCTCACTCTCAGACACT 366
DB 4838 GAGCTGGAAGATTTTGCAGTGTATCTGTACAGCACTATGTTAGTCTCACTCTCAGACACT 4891
QY 367 CAGATCACTTTCGGCGAGGAGCCAAAGGTGAGATCAAAAGCACTGTGTCAGCACTCT 426
DB 4892 -----TTGGCCAAAGGAGCAAGGTGGAACCTCAAAAGCACTGTGTCAGCACTCT 4942
QY 427 GTCT 430
DB 4943 GTCT 4946

RESULT 14
US-09-611-451-51
Sequence 51, Application US/09611451
Patent No. 6395275
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos F.
Lerner, Rignard A.
TITLE OF INVENTION: SYNTHETIC HUMAN NEUTRALIZING MONOCLONAL
ANTIBODIES TO HUMAN IMMUNODEFICIENCY VIRUS
NUMBER OF SEQUENCES: 92
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Scripps Research Institute, Office of
Patent Counsel
STREET: 10550 No. 6395275th Torrey Pines Road, TPC 8
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/611,451
FILING DATE: 06-Jul-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/591,632
FILING DATE: 2001-10-29
APPLICATION NUMBER: US 08/308,841
FILING DATE: 19-SEP-1994
APPLICATION NUMBER: US 08/233,619
FILING DATE: 26-APR-1994
APPLICATION NUMBER: US 08/139,409
FILING DATE: 19-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 332.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 784-2937
TELEFAX: (619) 784-9399
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 6166 base pairs
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-611-451-51

Query Match 34.7%; Score 318.4; DB 4; Length 6166;
Best Local Similarity 88.4%; Pred. No. 9.7e-81;
Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY 7 ATGAAAAAACCGCTATGCGGATCGCATGTCAGTGGCTGGTTCCTACCGTTGCCGAG 66
DB 4541 ATGAAAAAGACAGCTATGCGATTCAGTGGCAGTGGCTGGTTCCTACCGTTGCCGAG 4600
QY 67 GCCGATATTTGTTGACGAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAAAGAGCC 126
DB 4601 GCGG---CCGAGCTCAGCGAGTCTCCAGGCAACCTGCTTTGTCTCCAGGGGAAAGAGCC 4657
QY 127 ACCCTCTCTCGAGGGGCGAGTCAAGTGTAGTACAGCTTACCTTGTGTTACCAAGAG 186
DB 4658 ACCCTCTCTCGAGGGGCGAGTCAAGTGTAGTACAGGGGCTTACCTTGTGTTACCAAGAG 4717
QY 187 AAACCTGGCCAGGCTCCAGAGGCTCTCATCTATGTTGATCCACAGGGGCACTGGCAGT 246
DB 4718 AAACCTGGCCAGGCTCCAGAGGCTCTCATCTATGTTGATCCACAGGGGCACTGGCAGT 4777
QY 247 CCAGACAGGTTCAGTGGAGTGGTCCGGGACAGACTTCACTCTCACCATCAGTAGACTG 306
DB 4778 CCAGACAGGTTCAGTGGAGTGGTCTGGGACAGACTTCACTCTCACCATCAGTAGACTG 4837
QY 307 GAGCTGGAAGATTTTGCAGTGTATCTGTACAGCACTATGTTAGTCTCACTCTCAGACACT 366
DB 4838 GAGCTGGAAGATTTTGCAGTGTATCTGTACAGCACTATGTTAGTCTCACTCTCAGACACT 4891
QY 367 CAGATCACTTTCGGCGAGGAGCCAAAGGTGAGATCAAAAGCACTGTGTCAGCACTCT 426
DB 4892 -----TTGGCCAAAGGAGCAAGGTGGAACCTCAAAAGCACTGTGTCAGCACTCT 4942
QY 427 GTCT 430
DB 4943 GTCT 4946

RESULT 15
US-08-442-542-17
Sequence 17, Application US/08442542

Patent No. 5686600
GENERAL INFORMATION:
APPLICANT: Carozzi, Nadine B.
APPLICANT: Koziel, Michael G.
TITLE OF INVENTION: Antibodies which Bind to Insect Gut
TITLE OF INVENTION: Proteins and their Use
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ciba-Geigy Corporation
STREET: 7 Skyline Drive
CITY: Hawthorne
STATE: NY
COUNTRY: USA
ZIP: 10532
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,542
FILING DATE: 16-MAY-1995
CLASSIFICATION: 530
PRIORITY INFORMATION: 530
APPLICATION NUMBER: US 08/267,641
FILING DATE: 28-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Spruill, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: OGC 1750
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8615
TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 1797 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1797
OTHER INFORMATION: /note="381 single chain antibody"
OTHER INFORMATION: from pc184631"
US-08-442-542-17

Query Match 33.1%; Score 303.6; DB 1; length 1797;
Best Local Similarity 68.7%; Pred. No. 9.3e-77;
Matches 493; Conservative 0; Mismatches 189; Indels 36; Gaps 4;

QY 70 GATATTGTTGTCGAGTCGAGGACCCCTGCTTTGTCGAGGGGAAAGGCCACC 129
DB 67 GACATTGTGTCGACCGAGTCCTGCTTTGCTGTGCTGCTGCTGAGGGGACACC 126
QY 130 CTCTCTGAGGGGCGAGTCAGAGTGTAGT-----AGCAGTACTTACCTGCTGAC 180
DB 127 ATCTCTGAGAGCCGAGCGAAAGTGTGATCATATGACATTAAGTTTATGAACTGTTTC 186
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGAGCTCTCATCTATGTGTGATCCACAGGGCCACT 240
DB 187 CAACAGAAACAGGAGCAGCACCAGCAATCTCATCTATGTGTGATCCACAGGATCC 246
QY 241 GGCATCCGAGAGCTGTCAGTGTGTCAGTGTGTCGGGAGCAGACTTCCTCAGCATCAGT 300
DB 247 GGGGTCTCCGAGGTTTGTGTGTCAGTGTGTCGGGAGCAGACTTCAGCTCAGCATCAGT 306
QY 301 AGACTGAGCTGAGAGATTTTGCAGTGTATTACTGTGAGCAGTATGTAGTCACTCAG 360
DB 307 CCAATGAGAGAGATGATGATCTGCAATATTTTCTGTACGA-----AAGTAGG 354
QY 361 ACACTCAGATCACTTTGGCGGAGGAGCAGAGGTGAGATCAACGAACTGTGCTGCA 420

DB 355 GAACCTCCGTACACGTTGCGAGGGGAGACCAAGCTGGAATAAAGGGCTGATGCTGCA 414
QY 421 CCATCTGTCTGTGCGCGGAGGAGGCTTCGAGAGGTGTGATCAGGTGAGGTGCTCCAG 480
DB 415 CCAACTAGATCTGTGCGGCTGCGGCTGCGGCGGTGGTTC-----GCTGAGCAG 465
QY 481 GTGCACTGTGTGAGTCTGTGGGAGGCGGTGTGTCAGCTCTGGGAGGTCTCTGAGACTTCC 540
DB 466 GTCAACTGTGAGAGTCTGTGGAGATTTGTGCAAGCTTAAAGGTCATTGAAACTCTCA 525
QY 541 TGTGAGCTCTGGAATTCCTTCAGAACTTGTGATGATCAGTGTGCTCGGAGGCTCTA 600
DB 526 TGTGAGCTCTGGAATTCCTTCAGAACTTGTGATGATCAGTGTGCTCGGAGGCTCTCA 585
QY 601 GGCAGAGGCTGAGAGTGTGTCAGTGTATATATATATATGAGGCA-----CTAAATAC 654
DB 586 GGAAGAGGTTTGAATGGTTGCTGTGTCATTAAGAGTAAAGTAAATATATATGACATCT 645
QY 655 TACGCACTCTCGTGAAGGCGGATTCATCATCTCTCAGAGACACTTCCAAAGACAGGTG 714
DB 646 TATGCGATTCAGTGAAAGACAGTTCAACCGTCTCCAGAGATGATTCACAAAGCATGTTTC 705
QY 715 TATCTAAATATGAACAGCTGAGAACTGAGGACAGGCTGTCTATTACTGTGCGAGAG 772
DB 706 TATCTGCAATATGAACACTTGAAGAGGAGACAGCATGTATTACTGTGTAGGG 763

Search completed: September 17, 2003, 04:23:14
Job time : 68 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 03:49:20 ; Search time 871 Seconds
(without alignments)
2592.658 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918
Sequence: 1 GAATTCATCAAAAAACCGC.....ATCCACATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1660708 seqs, 122959015 residues

Total number of hits satisfying chosen parameters: 3321416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database: Published Applications NA.*

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2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq.*
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11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/1/pubpna/US09C_NEW_PUB.seq.*
13: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/1/pubpna/US10B_NEW_PUB.seq.*
16: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
17: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	918	100.0	918	11	US-09-782-397-13
2	916.4	99.8	918	11	US-09-782-397-15
3	799.6	87.1	867	11	US-09-782-397-16
4	798	86.9	867	11	US-09-782-397-18
5	361	39.2	450	11	US-09-782-397-6
6	359.4	39.2	450	11	US-09-782-397-4
7	324.4	35.3	543	11	US-09-782-397-1
8	324.4	35.3	543	11	US-09-782-397-3
9	319.8	34.8	1413	14	US-10-153-382-16
10	310.6	33.8	678	11	US-09-453-234-85
11	310.6	33.8	678	11	US-09-453-234-89
12	305.8	33.3	678	11	US-09-453-234-37
13	305.8	33.3	678	11	US-09-453-234-41
14	305.8	33.3	678	11	US-09-453-234-71
15	303.8	33.1	379	12	US-10-041-860-59
16	303.2	33.0	414	12	US-10-325-694-143

17	302.6	33.0	678	11	US-09-453-234-73	Sequence 73, Appl
18	302.2	32.9	379	12	US-10-041-860-67	Sequence 67, Appl
19	301	32.8	678	11	US-09-453-234-79	Sequence 79, Appl
20	301	32.8	948	10	US-09-859-053-33	Sequence 33, Appl
21	300.2	32.7	672	11	US-09-453-234-51	Sequence 51, Appl
22	299.8	32.6	708	14	US-10-153-382-6	Sequence 6, Appl
23	299.4	32.6	970	10	US-09-859-053-37	Sequence 37, Appl
24	297	32.4	672	11	US-09-453-234-39	Sequence 39, Appl
25	297	32.4	672	11	US-09-453-234-75	Sequence 75, Appl
26	295.4	32.2	357	12	US-10-226-615-3	Sequence 3, Appl
27	295.4	32.2	672	11	US-09-453-234-43	Sequence 43, Appl
28	295.4	32.2	672	11	US-09-453-234-77	Sequence 77, Appl
29	295.2	32.2	367	12	US-10-330-613-31	Sequence 31, Appl
30	295.2	32.2	367	12	US-10-330-530-31	Sequence 13125, A
31	293.4	32.0	961	14	US-10-198-846-11125	Sequence 16611, A
32	292.8	31.9	413	11	US-09-918-995-16641	Sequence 60, Appl
33	292	31.8	1184	14	US-10-158-646-60	Sequence 66, Appl
34	291.8	31.8	1458	14	US-10-158-646-66	Sequence 64, Appl
35	290.2	31.6	1775	14	US-10-158-646-64	Sequence 99, Appl
36	288.6	31.4	645	11	US-09-972-656-99	Sequence 89, Appl
37	287.4	31.3	378	11	US-09-848-798-95	Sequence 48, Appl
38	287.2	31.3	723	12	US-10-127-890-89	Sequence 57, Appl
39	287	31.3	645	11	US-09-791-153A-48	Sequence 75, Appl
40	286.8	31.2	1202	14	US-10-158-646-57	Sequence 230, App
41	286.4	31.2	382	12	US-10-041-860-75	Sequence 94, Appl
42	286	31.2	375	11	US-09-848-798-194	
43	285.2	31.1	1798	9	US-09-925-299-230	
44	285.2	31.1	1798	11	US-09-925-299-230	
45	284.2	31.0	378	11	US-09-848-798-94	

ALIGNMENTS

RESULT 1
US-09-782-397-13
Sequence 13, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Mailli, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: leinhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792


```

; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..906, 913..918)
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-782-397-13

Query Match      100.0%; Score 918; DB 11; Length 918;
Best Local Similarity 100.0%; Pred. No. 7,6e-270;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Oy      1  GAATTCATGAAAAAACCAGCTATGCGATGCGAGTTGCACTGGCTGGTTTGGCTAACCGTT 60
Db      1  GAATTCATGAAAAAACCAGCTATGCGATGCGAGTTGCACTGGCTGGTTTGGCTAACCGTT 60

Oy      61  GCGAGGCGCGAATATGTTGTTGACGAGCTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120
Db      61  GCGAGGCGCGAATATGTTGTTGACGAGCTCCAGGACCCCTGCTTGTCTCCAGGGGAA 120

Oy      121  AGAGCACCCTCTCTCTGACGGGCGCAGTCAAGTGTATTAGACGACTACTTACCTGTGAC 180
Db      121  AGAGCACCCTCTCTCTGACGGGCGCAGTCAAGTGTATTAGACGACTACTTACCTGTGAC 180

Oy      181  CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCTCATCTATGTGTGATCCACAGGGCACT 240
Db      181  CAGCAGAAAACCTGGCCAGGCTCCAGGCTCTCTCATCTATGTGTGATCCACAGGGCACT 240

Oy      241  GGCATGCCCGAAGAGTTCAGTGGCAGTGGGTCGGGAGACAGCTTCACTCCAACTCACT 300
Db      241  GGCATGCCCGAAGAGTTCAGTGGCAGTGGGTCGGGAGACAGCTTCACTCCAACTCACT 300

Oy      301  AGACTGAGGCTGAAGATTTTGCAGTGTATTAAGTCAAGATATGTATGTACCTCACTCAG 360
Db      301  AGACTGAGGCTGAAGATTTTGCAGTGTATTAAGTCAAGATATGTATGTATGTACCTCAG 360

Oy      361  ACACTTCAGATCACTTTCCGCGGAGGAGCCAAAGTGTGAGATCAAAAGAACTGTGGTGA 420
Db      361  ACACTTCAGATCACTTTCCGCGGAGGAGCCAAAGTGTGAGATCAAAAGAACTGTGGTGA 420

Oy      421  CCATCTGTCTCGGGGCGGTGGCGGTTCCGAGGAGGTGATCAAGTGTGAGAGTGGGCTCCAG 480
Db      421  CCATCTGTCTCGGGGCGGTGGCGGTTCCGAGGAGGTGATCAAGTGTGAGAGTGGGCTCCAG 480

Oy      481  GTGCAGCTGTGGAGTCTGGGGGAGGCGTGTCTCAAGCTGGAGAGTCCCTGAGACTCTCC 540
Db      481  GTGCAGCTGTGGAGTCTGGGGGAGGCGTGTCTCAAGCTGGAGAGTCCCTGAGACTCTCC 540

Oy      541  TGTGCAAGCTCTGGAATTCCTCTTCAGAACTTTGCTATGCACTGGGTCGGCCAGGCTCTA 600
Db      541  TGTGCAAGCTCTGGAATTCCTCTTCAGAACTTTGCTATGCACTGGGTCGGCCAGGCTCTA 600

Oy      601  GGCAAGGGGCTGGAAGTGGGAGTATATATCAATATGATGGAAGCACTAAATCTACACGA 660
Db      601  GGCAAGGGGCTGGAAGTGGGAGTATATATCAATATGATGGAAGCACTAAATCTACACGA 660

Oy      661  GACTCCGTGAAGGCGCATTCACCATCTCCAGAGCACTTCCAAAGAACGGGTATCTTA 720
Db      661  GACTCCGTGAAGGCGCATTCACCATCTCCAGAGCACTTCCAAAGAACGGGTATCTTA 720

Oy      721  AAAATGACAAGCTTGAACTGAGACAAGGCTGTCTATTACTGTCTCGAGAGATCAAGAC 780
Db      721  AAAATGACAAGCTTGAACTGAGACAAGGCTGTCTATTACTGTCTCGAGAGATCAAGAC 780

Oy      781  CTGTTGGGGGACATATACAATACTAAGGTTTGGAGGTCGGGGGCAAAAGGACCAAGGTC 840
Db      781  CTGTTGGGGGACATATACAATACTAAGGTTTGGAGGTCGGGGGCAAAAGGACCAAGGTC 840

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QY 841 ACCGTCCTCAGGATCCGAACAAACTGATCAGCGAAGAAGATCTGAACATCCCAT 900
DB 841 ACCGTCCTCAGGATCCGAACAAACTGATCAGCGAAGAAGATCTGAACATCCCAT 900
QY 901 CACCATTAGTGAAAGCTT 918
DB 901 CACCATTAGTGAAAGCTT 918

RESULT 2
US-09-782-397-15/c
Sequence 15, Application US/09782397
Publication No. US20030021799A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Maiti, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-782-397-15

Query Match 99.8%; Score 916.4; DB 1; Length 918;
Best Local Similarity 99.9%; Pred. No. 2,4e-269;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCATGAAAAAACCAGCTATCGCATCGCAGTTGCACTGGCTTGGCTACCGTT 60
DB 918 GAATTCATGAAAAAACCAGCTATCGCATCGCAGTTGCACTGGCTTGGCTACCGTT 859
QY 61 GCGCAGGCCGATATTGTGTGACGCGAGTCTCCAGGCAACCTGTCTTTGTCTCCAGGGGAA 120
DB 858 GCGCAGGCCGATATTGTGTGACGCGAGTCTCCAGGCAACCTGTCTTTGTCTCCAGGGGAA 799
QY 121 AGAGCACCCTCTCCTGCGAGGGCCAGTCAGAGTGTAGTAGCAGCACTTAGCGTGTAC 180
DB 798 AGAGCACCCTCTCCTGCGAGGGCCAGTCAGAGTGTAGTAGCAGCACTTAGCGTGTAC 739

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QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 240
DB 738 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 679
QY 241 GGCATGCCGACGAGGCTTGGAGTGGGTCCGGGACAGACTTCACTCTCAGCAGT 300
DB 678 GGCATGCCGACGAGGCTTGGAGTGGGTCCGGGACAGACTTCACTCTCAGCAGT 619
QY 301 AGACTGAGCCTGAGATTTTTCAGTGTATTACTGTACAGATGATGATGATGATGATGAT 360
DB 618 AGACTGAGCCTGAGATTTTTCAGTGTATTACTGTACAGATGATGATGATGATGATGAT 559
QY 361 ACACCTCAGATCACTTTCGGGAGGAGCCAGAGTGGAGATCAAGAGAGAGTGGTGGTGA 420
DB 558 ACACCTCAGATCACTTTCGGGAGGAGCCAGAGTGGAGATCAAGAGAGAGTGGTGGTGA 499
QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
DB 498 CCATCTGTCTCTGGCGGTGGCGGTTCGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 439
QY 481 GTGCAGCTGTGTAGTCTGGGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 438 GTGCAGCTGTGTAGTCTGGGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 379
QY 541 GTGCAGCTGTGTAGTCTGGGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 600
DB 378 GTGCAGCTGTGTAGTCTGGGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 319
QY 601 GGCAGAGGCTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 660
DB 318 GGCAGAGGCTGTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 259
QY 661 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACCTTCCAGAGAGCGGTATCTTA 720
DB 258 GACTCCGTGAGAGGCGGATTCACCATCTCCAGAGACCTTCCAGAGAGCGGTATCTTA 199
QY 721 AAATGAGAGGCTGTGTAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 780
DB 198 AAATGAGAGGCTGTGTAGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 139
QY 781 CTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 840
DB 138 CTGTGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 79
QY 841 ACCGTCTCTCAGGATCCGAGCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 900
DB 78 ACCGTCTCTCAGGATCCGAGCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 19
QY 901 CACCATTTAGTGAAGCTT 918
DB 18 CACCATTTAGTGAAGCTT 1

RESULT 3
US-09-782-397-16
; Sequence 16, Application us/09782397
; Publication No. US20030021779A1
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maiti, Pradip K.
; Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESS: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..855, 862..867)
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-782-397-16

Query Match 87.1%; Score 799.6; DB 11; Length 867;
Best Local Similarity 94.0%; Pred. No. 1e-233;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATTCGATCGAGTTCAGTGGCTGTGCTACCGTT 60
DB 1 GAATTCATGAAAAAACCCTATTCGATCGAGTTCAGTGGCTGTGCTACCGTT 60
QY 61 GGCAGAGCGGATATGTGTGTGACGAGTGTCCAGAGCACTGTCTTGTCTCCAGGGAA 120
DB 61 GGCAGAGCGGATATGTGTGTGACGAGTGTCCAGAGCACTGTCTTGTCTCCAGGGAA 120
QY 121 AAGGCCACCTCTCTGTGAGGCGCAGTCAAGTGTGAGCAAGCTACTTAAGCTGTAC 180
DB 121 AAGGCCACCTCTCTGTGAGGCGCAGTCAAGTGTGAGCAAGCTACTTAAGCTGTAC 180
QY 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 240
DB 181 CAGCAGAAACCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCTACT 240
QY 241 GGCATGCCGACGAGGCTTGGAGTGGGTCCGGGACAGACTTCACTCTCAGCAGT 300
DB 241 GGCATGCCGACGAGGCTTGGAGTGGGTCCGGGACAGACTTCACTCTCAGCAGT 300
QY 301 AGACTGAGCCTGAGATTTTTCAGTGTATTACTGTACAGATGATGATGATGATGATGAT 360
DB 301 AGACTGAGCCTGAGATTTTTCAGTGTATTACTGTACAGATGATGATGATGATGATGAT 360
QY 361 ACACCTCAGATCACTTTCGGGAGGAGCCAGAGTGGAGATCAAGAGAGAGTGGTGGTGA 420
DB 361 ACACCTCAGATCACTTTCGGGAGGAGCCAGAGTGGAGATCAAGAGAGAGTGGTGGTGA 420
QY 421 CCATCTGTCTCTGGCGGTGGCGGTTCGGGAGTGGTGGTGGTGGTGGTGGTGGTGGTGG 480
DB 421 TC-----CGAGCAG 429
QY 481 GTGCAGCTGTGTAGTCTGGGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
DB 430 GTGCAGCTGTGTAGTCTGGGAGGAGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 489

QY 541 TGTGAGGCTCTGAGATTCCTCCCTTCAAGAGCTTTGCTATGCACTGGGTCGCCAGGCTCTA 600
 Db 490 TGTGAGGCTCTGAGATTCCTCCCTTCAAGAGCTTTGCTATGCACTGGGTCGCCAGGCTCTA 549
 QY 601 GGCAGAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGAGCACTAAATACACCA 660
 Db 550 GGCAGAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGAGCACTAAATACACCA 609
 QY 661 GACTCCGTGAGAGGGGCTGATTCACCATCTCCAGAGCACTTCCAGAGCAAGCGGTATCTA 720
 Db 610 GACTCCGTGAGAGGGGCTGATTCACCATCTCCAGAGCACTTCCAGAGCAAGCGGTATCTA 669
 QY 721 AAATGAGACAGGCTGAGACTGAGAGCAAGCGGTCTATTACTGTGGAGAGATCAAGC 780
 Db 670 AAATGAGACAGGCTGAGACTGAGAGCAAGCGGTCTATTACTGTGGAGAGATCAAGC 729
 QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCTC 840
 Db 730 CTGTGGGTGACTATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCTC 789
 QY 841 ACCGTCTCTCAGAGTCCGAGCAAAACTGATCAGCGAAGAGATCTGAACATCACAT 900
 Db 790 ACCGTCTCTCAGAGTCCGAGCAAAACTGATCAGCGAAGAGATCTGAACATCACAT 849
 QY 901 CACCATTAAGTGAAGCTT 918
 Db 850 CACCATTAAGTGAAGCTT 867

RESULT 4
 US-09-782-397-18/c
 ; Sequence 18, Application US/09782397
 ; Publication No. US20030021779A1

GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 Mailli, Pradip K.
 Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
 SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
 DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/782,397

FILING DATE: 13-Feb-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/862,124

FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 18:

SEQUENCE CHARACTERISTICS:

LENGTH: 867 base pairs

TYPE: nucleic acid

STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 US-09-782-397-18

Query Match 86.9%; Score 798; DB 11; Length 867;
 Best Local Similarity 93.9%; Pred. No. 3.2e-233;
 Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

QY 1 GAATTCATGAAAAAACCCTATCGCATGCAAGTTGCACTGGCTGTTTGGCTACCGTT 60
 Db 867 GAATTCATGAAAAAACCCTATCGCATGCAAGTTGCACTGGCTGTTTGGCTACCGTT 808
 QY 61 GCCGAGGCCGATATTTGTTTGAAGCACTCTCCAGGCACTCTGTTTGTCTCCAGGGAA 120
 Db 807 GCCGAGGCCGATATTTGTTTGAAGCACTCTCCAGGCACTCTGTTTGTCTCCAGGGAA 748
 QY 121 AGAGCCACCTCTCTCCAGAGGCGAGTCAAGAGTTAGTACAGCTACTAGCGTGTAC 180
 Db 747 AGAGCCACCTCTCTCCAGAGGCGAGTCAAGAGTTAGTACAGCTACTAGCGTGTAC 688
 QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCACT 240
 Db 687 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGCGCACT 628
 QY 241 GGCATGCCAGACAGTTTCACTGAGTGGTCCGCGACAGACTTCACTCTCAACATCACT 300
 Db 627 GGCATGCCAGACAGTTTCACTGAGTGGTCCGCGACAGACTTCACTCTCAACATCACT 568
 QY 301 AGACTGAGGCTGAAAGATTTTGAGTGTATCTGTCAAGATGATGATGATGATGATGAT 360
 Db 567 AGACTGAGGCTGAAAGATTTTGAGTGTATCTGTCAAGATGATGATGATGATGATGAT 508
 QY 361 ACACTCAGATCACTTTCCGCGAGGACCAAGGTGAGATCAAGAACTGTGGCTGCA 420
 Db 507 ACACTCAGATCACTTTCCGCGAGGACCAAGGTGAGATCAAGAACTGTGGCTGCA 448
 QY 421 CCAATGCTCTGCGCGGTGGCGGTTCCGAGAGTGTGATCAAGTGGAGTGGTCCCGAG 480
 Db 447 TC-----CGACAG 439
 QY 481 GTGCACTGTGAGTCTGCGGAGGCGGTGTCACGCTGGAGGATCCCTGAGACTCTCC 540
 Db 438 GTGCACTGTGAGTCTGCGGAGGCGGTGTCACGCTGGAGGATCCCTGAGACTCTCC 379
 QY 541 TGTGCAAGCTCTGAGATTCCTCTTCAAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 600
 Db 378 TGTGCAAGCTCTGAGATTCCTCTTCAAGAGCTTTGCTATGCACTGGTCCGCAAGCTCTA 319
 QY 601 GGCAGAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGAGCACTAAATACACCA 660
 Db 318 GGCAGAGGGGCTGAGTGGGTGGGCTGATATATCATATGATGAGAGCACTAAATACACCA 259
 QY 661 GACTCCGTGAGAGGGGCTGATTCACCATCTCCAGAGCACTTCCAGAGCAAGCGGTATCTA 720
 Db 258 GACTCCGTGAGAGGGGCTGATTCACCATCTCCAGAGCACTTCCAGAGCAAGCGGTATCTA 199
 QY 721 AAATGAGACAGGCTGAGAACTGAGAGCAAGGCTGTATTACTGTGCGAGAGATCAGAGC 780
 Db 198 AAATGAGACAGGCTGAGAACTGAGAGCAAGGCTGTATTACTGTGCGAGAGATCAGAGC 139
 QY 781 CTGTGGGTGACTATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCGTCT 840
 Db 138 CTGTGGGTGACTATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCGTCT 79
 QY 841 ACCGTCTCTCAGAGTCCGAGCAAAACTGATCAGCGAAGAGATCTGAACATCACAT 900
 Db 78 ACCGTCTCTCAGAGTCCGAGCAAAACTGATCAGCGAAGAGATCTGAACATCACAT 19
 QY 901 CACCATTAAGTGAAGCTT 918
 Db 18 CACCATTAAGTGAAGCTT 1

RESULT 5
US-09-782-397-6/c
Sequence 6, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Maiti, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-782-397-6

Query Match 39.3%; Score 361; DB 11; Length 450;
Best Local Similarity 100.0%; Pred. No. 66-100;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 129
DB 378 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 319
QY 130 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGGAAA 189
DB 318 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGGAAA 259
QY 190 CCTGCGCAGGCTCCAGGCTCCTCATCTATGAGTCATCCAGGAGCCACTGGCATGCCA 249
DB 258 CTGCGCAGGCTCCAGGCTCCTCATCTATGAGTCATCCAGGAGCCACTGGCATGCCA 199
QY 250 GACAGTTCACTGAGTGGGTCGGGAGACAGCTTCACTTCACTCACTAGTAGAG 309
DB 198 GACAGTTCACTGAGTGGGTCGGGAGACAGCTTCACTTCACTCACTAGTAGAG 139
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCACTATGAGTCACTCAGACACTCAG 369
DB 138 CCTGAAGATTTTGCAGTGTATTACTGTCAAGCACTATGAGTCACTCAGACACTCAG 79

QY 370 ATCACTTTGGCGGAGGAGCAAGTGAATCAACGAAGTGTGCTGCACCATCTGTC 429
DB 78 ATCACTTTGGCGGAGGAGCAAGTGAATCAACGAAGTGTGCTGCACCATCTGTC 19
QY 430 T 430
DB 18 T 18

RESULT 6
US-09-782-397-4
Sequence 4, Application US/09782397
Publication No. US20030021779A1
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Maiti, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 450 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 1..450
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-782-397-4

Query Match 39.2%; Score 359.4; DB 11; Length 450;
Best Local Similarity 99.7%; Pred. No. 1.9e-99;
Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 129
DB 72 GATATTGTTGACGAGCTCTCCAGGACCCCTGTTTGTCTCCAGGGGAAAGAGCCACC 132
QY 130 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGGAAA 189
DB 133 CTCTCTGAGGGCCAGTGAAGTGTAGTGAAGAGCTACTTACCTGSTRACCGAGGAAA 192

Qy	190	CTGGCCAGGCTCCGAGGCTCCATCTAATGGTGATCCA	CGAGGCGCACTGGGATGCCA	249
Db	193	CTGGCCAGGCTCCGAGGCTCCATCTAATGGTGATCCA	CGAGGCGCACTGGGATGCCA	252
Qy	250	GACAGTTTCACTGGCAGTGGGTCCGGGACAGACTTCACTTCA	CCATCATGTAGCTGGAG	309
Db	253	GACAGGTCGAGTGGCAGTGGGTCCGGGACAGACTTCACTTCA	CCATCATGTAGCTGGAG	312
Qy	310	CTGAAGATTTCAGTGTATTACTGTACAGATATGGAGTCA	CCCTCAGACCTTCAG	369
Db	313	CTGAAGATTTCAGTGTATTACTGTACAGATATGGAGTCA	CCCTCAGACCTTCAG	372
Qy	370	ATCACTTTCGCGGAGGGAACAAAGTGAAGTCAACGAACTGTGGCTGC	ACCATCTGTC	429
Db	373	ATCACTTTCGCGGAGGGAACAAAGTGAAGTCAACGAACTGTGGCTGC	ACCATCTGTC	432
Qy	430	T	430	
Db	433	T	433	

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1      RESULT 7
2      US-09-782-397-1
3      Sequence 1, Application US/097823397
4      Publication No. US20030021779A1
5      GENERAL INFORMATION:
6      APPLICANT: Dan, Michael D.
7      Malti, Pradip K.
8      Kaplan, Howard A.
9      TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
10     SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
11     FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
12     DETECTION OF CANCERS
13     NUMBER OF SEQUENCES: 28
14     CORRESPONDENCE ADDRESS:
15     ADDRESSEE: Morrison & Foerster LLP
16     STREET: 755 Page Mill Road
17     CITY: Palo Alto
18     STATE: CA
19     COUNTRY: USA
20     ZIP: 94304-1018
21     COMPUTER READABLE FORM:
22     MEDIUM TYPE: Floppy disk
23     COMPUTER: IBM PC compatible
24     OPERATING SYSTEM: PC-DOS/MS-DOS
25     SOFTWARE: PatentIn Release #1.0, Version #1.30
26     CURRENT APPLICATION DATA:
27     APPLICATION NUMBER: US/09/782,397
28     FILING DATE: 13-Feb-2001
29     CLASSIFICATION: <Unknown>
30     PRIOR APPLICATION DATA:
31     APPLICATION NUMBER: 08/862,124
32     FILING DATE: 1997-05-22
33     ATTORNEY/AGENT INFORMATION:
34     NAME: Lehnhardt, Susan K.
35     REGISTRATION NUMBER: 33,943
36     REFERENCE/DOCKET NUMBER: 31608-20001.20
37     TELECOMMUNICATION INFORMATION:
38     TELEPHONE: (650) 813-5600
39     TELEFAX: (650) 494-0792
40     TELEX: 706141
41     INFORMATION FOR SEQ ID NO: 1:
42     SEQUENCE CHARACTERISTICS:
43     LENGTH: 543 base pairs
44     TYPE: nucleic acid
45     STRANDEDNESS: double
46     TOPOLOGY: linear
47     FEATURE:
48     NAME/KEY: CDS
49     LOCATION: 1..543
50     SEQUENCE DESCRIPTION: SEQ ID NO: 1:
51     US-09-782-397-1

```

Query Match	35.3%	Score 324.4;	DB 11;	Length 543;
Best Local Similarity	89.3%;	Pred. No. 9.5e-89;		
Matches 349; Conservative	0;	Mismatches 42;	Indels 0;	Gaps 0;

Qy	440	GGCGTTCCGGAGAGTGGATCAGGTGGAGGGAGGCTCCAGATGCAGCTGGTGGAGCTG	499
Db	152	GGGTTTCTCGTGTGCTCTTTTAAAGAGTATCCAGTGCAGGTGCAGCTGGTGGAGCTG	211
Qy	500	GGGAGAGCGTGGTCCAGCCTGGAGAGTCCCTGAGACTCTCTGTCAGACCTCTGGATTCC	559
Db	212	GGGAGAGCGGTGGTCCAGCCTGGAGAGTCCCTGAGACTCTCTGTCAGACCTCTGGATTCC	271
Qy	560	CCCTTGAAAGCTTTTGCTATGCATCGGGTCCGCGCAGGCTCTTAGGCAAGGGCTGGAGTGGG	619
Db	272	CCCTTGAAAGCTTTGCTATGCATCGGGTCCGCGCAGGCTCTTAGGCAAGGGCTGGAGTGGG	331
Qy	620	TGGCAGTTATCATATGATGGAGACCTAAATATCTACGACGACTCCGTGAAGGGCCGAT	679
Db	332	TGGCAGTTATCATATGATGGAGACCTAAATATCTACGACGACTCCGTGAAGGGCCGAT	391
Qy	680	TCACCATCTCCAGAGACATTCGCAAGAACGAGGTGTCTTAAATGAACGCTGAGAA	739
Db	392	TCACCATCTCCAGAGACATTCGCAAGAACGAGGTGTCTTAAATGAACGCTGAGAA	451
Qy	740	CTGAGGACCGGCTGTCTATTACTGTGCGAAGATCAGAGCTCTTGGGTGACTATGACC	799
Db	452	CTGAGGACCGGCTGTCTATTACTGTGCGAAGATCAGAGCTCTTGGGTGACTATGACC	511
Qy	800	ACTACTAGCGTTGGACGCTGGGGCAAAAG	830
Db	512	ACTACTAGCGATTGGACGCTTGGGGAAAGG	542

RESULT 8
 US-09-782-397-3/c
 Sequence 3, Application US/09782397
 Publication No. US20030021779A1
 GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 Maici, Pradipl K.
 Kaplan, Howard A.
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT
 SPECIFICALLY DETECT CANCER CELLS, NOCLOETIDES ENCODING THEM
 FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
 DETECTION OF CANCERS
 NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster LLP
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/782,397
 FILING DATE: 13-Feb-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/862,124
 FILING DATE: 1997-05-22
 ATTORNEY/AGENT INFORMATION:
 NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 31608-20001.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792

```

1 TELEX: 706141
2
3 INFORMATION FOR SEQ ID NO: 3:
4
5 SEQUENCE CHARACTERISTICS:
6     LENGTH: 543 base pairs
7     TYPE: nucleic acid
8     STRANDEDNESS: double
9     TOPOLOGY: linear
10
11 SEQUENCE DESCRIPTION: SEQ ID NO: 3:
12
13 US-09-762-357-3

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Query Match	35.3%;	Score 324.4;	DB 11;	Length 543;
Best Local Similarity	89.3%;	Pred. No. 9.5e-89;		
Matches 349;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;

Qy	440	GCGGTTCGGAGAGGTGTGGATCAGAGTGAAGAGTGGCTCCCAAGTGACAGCTGGTGGAGACTG	459
Db	392	GGGTTTTTCCTCGTTGCTCTTTTAAAGAGTATCCATGTCAGGTGCAGCTGGTGGAGTCTG	333
Qy	500	GGGAGAGCGTGGTGCACGCTGGAGGTCCTTGAGACTCTCTGTGCAAGCTCTTGGATTCC	555
Db	332	GGGAGAGCGTGGTGCACGCTGGAGGTCCTTGAGACTCTCTGTGCAAGCTCTTGGATTCC	273
Qy	560	CTTTCAGAAAGCTTTCCTATGCACTGGGTCCGCCAAGCTCTTAGGCMAAGGAGCTGGAGTGGG	619
Db	272	CTTTCAGAAAGCTTTCCTATGCACTGGGTCCGCCAAGCTCTTAGGCMAAGGAGCTGGAGTGGG	213
Qy	620	TGGCAGTTATATCATATGATGGAGCACTAAATATCAAGCAAGCTCCGTTGAAGGGCCGAT	679
Db	212	TGGCAGTTATATATATGATGGAGCACTAAATATCAAGCAAGCTCCGTTGAAGGGCCGAT	153
Qy	680	TCAACATCTTCAGAGACACTTCCAGAGAACCGGTATCTTAAATGAACAGCTTGAGAA	739
Db	152	TCAACATCTTCAGAGACACTTCCAGAGAACCGGTATCTTAAATGAACAGCTTGAGAA	93
Qy	740	CTGAGGACACGGCTGTCTATTTACTGTGCGAGATCAAGACCTGTTGGGTGATATGACC	799
Db	92	CTGAGGACACGGCTGTCTATTTACTGTGCGAGATCAAGACCTGTTGGGTGATATGACC	33
Qy	800	ACTACTACGGTTTGAACGTCTGGGGCAAAAG	830
Db	32	ACTACTACGGTTTGAACGTCTGGGGCAAAAG 2	

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RESULT 9
US-10-153-382-16
: Sequence 16, Application US/10153382
: Publication No. US20030086930A1
: GENERAL INFORMATION:
: APPLICANT: PFIZER PRODUCTS INC.
: TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
: FILE REFERENCE: PCG3019A
: CURRENT APPLICATION NUMBER: US/10/153,382
: CURRENT FILING DATE: 2002-05-22
: PRIOR APPLICATION NUMBER: 60/293042
: PRIOR FILING DATE: 2001-05-23
: NUMBER OF SEQ ID NOS: 39
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 16
: LENGTH: 1413
: TYPE: DNA
: ORGANISM: Homo sapiens
: US-10-153-382-16

```

```

Query Match      34.8%; Score 319.8; DB 14; Length 1413;
Best Local Similarity 85.2%; Pred. No. 3.3e-87;
Matches 351; Conservative 0; Mismatches 62; Indels 0; Gaps 0

QY      440 GCGGTTCCGAGAGTGTGTGATCAGGTGAGAGGCTCCAGATGACAGCTGTGTGAGCTG 439
Db      20 GGGTTTTCCTCGTGTCTCTTTTAAGAGGATGTCACATGTCAGGTGACAGCTGTGTGAGCTG 79

QY      500 GGGGAGCGGTGTGTCAGCTGGGAGGTCCCTGAGACTCTCTGTGCAAGCTCTGTGATTCC 559

```

Db	8	GGGGAAGCGTGGATCCAGCGCTGGAGAGTCCCTTGAGACATCCCTGTGACAGCGCTGGATTCA	129
Qy	560	CCTTCGAAAGCTTTGCTATGACATGGGTTCCGCAAGGCTCTTAGGCAAGGGGCTGAGTGGG	619
Db	140	CTTCAGTAGCATGATGGCATGCACTGGGTGCCCAAGGCTCCAGGCAAGGGGCTGAGTGGG	199
Qy	620	TGGCAATTATCATATGATGGAGCACTAAATCTACGCAATCCGTTCAAGGCCAT	679
Db	200	TGGCAATTATATGATGATGATGGAGTATTAATATCTATGCAATCCGTTCAAGGCCAT	259
Qy	680	TACCATCTCCGAGAGACACTTCCAGAACAGGGTGTATCTTAAATGAAACGCTTGAA	739
Db	260	TACCATCTCCGAGAGACACTTCCAGAACAGGGTGTATCTGCAATGAATAAACGCTTGAG	319
Qy	740	CTGAGGACACGGCTGTCTAATTACTGTGCGAGAGATCAAGGCTTTGGGTGACATTAGCC	799
Db	320	CGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGAAGGAGACTAACCTTTAATACT	379
Qy	800	ACTACTACGGTTTGAACGCTGGGGCAAGGAGCAAGGTCAACGTTCTCCAGATACC	858
Db	380	ACTACTACGGTATGAGACGCTGGGGCAAGGAGCAAGGTCAACGTTCTCCAGACCTCC	438

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RESULT 10
US-09-453-234-49
; Sequence 49, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Valkirs, Gnnars
; APPLICANT: Gray, Jeff
; APPLICANT: Lombey, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; PRIOR FILING DATE: 1999-10-02
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: M1-23L
; NAME/KEY: CDS
; LOCATION: (1)..(678)
US-09-453-234-49

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Query Match	33.8%	Score 310.6;	DB 11;	Length 678;
Best Local Similarity	93.6%;	Pred. No. 1.7e-84;		
Matches 338;	Conservative 0;	Mismatches 14;	Indels 9;	Gaps 1

QY	7G	GAATATGTTATGACAGATCTCCAGGACACCTGTCTTTGTCTCCAGGGGAAAGGCACC	129
Db	1	GAATATGTTATGACAGATCTCCAGGACACCTGTCTTTGTCTCCAGGGGAAAGGCACC	60
QY	130	CTCTCTCCGACAGGGCCAGTCAAGATGTTAGTAGCAGCTATTAGCTTGATCCAGCAGAA	189
Db	61	CTCTCTCCGACAGGGCCAGTCAAGATGTTAGTAGCAGCTATTAGCTTGATCCAGCAGAA	120
QY	190	CCTGGCAGAGCTCCAGGCTCTCATCTATAGTGCATTCACAGGGGCATGGCAGTGGCA	249
Db	121	CCTGGCAGAGCTCCAGGCTCTCATCTATAGTGCATTCACAGGGGCATGGCAGTGGCA	180
QY	250	GACAGGTTCAGTGGCAGTGGGTCCGGGACAGACTTCACTCTCACATCACTAGACCTGGAG	309
Db	181	GACAGGTTCAGTGGCAGTGGGTCTGGGACAGACTTCACTCTCACATCACTAGACCTGGAG	240
QY	310	CCTGAAGATTTTCAGATGATTAATCTGTACAGCAGTAGGTAGCTCACTCAGACACTCAG	369

Db 241 CCTGAAGATTGTCAGTGTATTACTGTCTGACGAGTATGGTAGCT-----CACCTTCG 291
Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTGCACCATCTGTC 429
Db 292 TACACTTTGGCGGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTGCACCATCTGTC 351
Qy 430 T 430
Db 352 T 352

RESULT 11
US-09-453-234-85
; Sequence 85, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 85
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(678)
; OTHER INFORMATION: M2-33L
US-09-453-234-85

Query Match 33.8%; Score 310.6; DB 11; Length 678;
Best Local Similarity 93.6%; Pred. No. 1.7e-84;
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

Qy 70 GATATTGTTGAGCGAGTCTCCAGGCACTCTGTTCTTCTCCAGGGGAAAGGCCACC 129
Db 1 GAAATGTGTGAGCGAGTCTCCAGGCACTCTGTTCTTCTCCAGGGGAAAGGCCACC 60
Qy 130 CTCTCCTGCGAGGCGCAGTCAAGTGTAGTAGAGCTACTAGGCTGGTACACAGAGAAA 189
Db 61 CTCTCCTGCGAGGCGCAGTCAAGTGTAGTAGAGCTACTAGGCTGGTACACAGAGAAA 120
Qy 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCACAGGCGCACTGGGATGCCA 249
Db 121 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCACAGGCGCACTGGGATGCCA 180
Qy 250 GACAGGTTCAAGTGGAGTGGGTCCGGGACAGACTTCACTTCAACATGATGAAGTGGAG 309
Db 181 GACAGGTTCAAGTGGAGTGGGTCTGGGACAGACTTCACTTCAACATGAGGAGCTGGAG 240
Qy 310 CCTGAAGATTTTGGAGTGTATTACTGTGAGAGTATGGTAGCTCAACCTCAGAGCACTCAG 369
Db 241 CCTGAAGATTTTGGAGTGTATTACTGTGAGAGTATGGTAGCT-----CACCTTCG 291
Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTGCACCATCTGTC 429
Db 292 TACACTTTGGCGGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTGCACCATCTGTC 351
Qy 430 T 430
Db 352 T 352

RESULT 12
US-09-453-234-37
; Sequence 37, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.
; APPLICANT: Genpharm International
; TITLE OF INVENTION: Human Antibodies
; FILE REFERENCE: 020015-000110US
; CURRENT APPLICATION NUMBER: US/09/453,234
; PRIOR FILING DATE: 1999-12-01
; PRIOR APPLICATION NUMBER: US 60/157,415
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(678)
US-09-453-234-37

Query Match 33.3%; Score 305.8; DB 11; Length 678;
Best Local Similarity 92.8%; Pred. No. 4.9e-83;
Matches 335; Conservative 0; Mismatches 17; Indels 9; Gaps 1;

Qy 70 GATATTGTTGAGCGAGTCTCCAGGCACTCTGTTCTTCTCCAGGGGAAAGGCCACC 129
Db 1 GAAATGTGTGAGCGAGTCTCCAGGCACTCTGTTCTTCTCCAGGGGAAAGGCCACC 60
Qy 130 CTCTCCTGCGAGGCGCAGTCAAGTGTAGTAGAGCTACTTACCTGGTACACAGAGAAA 189
Db 61 CTCTCCTGCGAGGCGCAGTCAAGTGTAGTAGAGCTACTTACCTGGTACACAGAGAAA 120
Qy 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCACAGGCGCACTGGGATGCCA 249
Db 121 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCACAGGCGCACTGGGATGCCA 180
Qy 250 GACAGGTTCAAGTGGAGTGGGTCCGGGACAGACTTCACTTCAACATGATGAAGTGGAG 309
Db 181 GACAGGTTCAAGTGGAGTGGGTCTGGGACAGACTTCACTTCAACATGAGGAGCTGGAG 240
Qy 310 CCTGAAGATTTTGGAGTGTATTACTGTGAGAGTATGGTAGCTCAACCTCAGAGCACTCAG 369
Db 241 CCTGAAGATTTTGGAGTGTATTACTGTGAGAGTATGGTAGCT-----CACCTTCA 291
Qy 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTGCACCATCTGTC 429
Db 292 TACACTTTGGCGGAGGAGCAAGGTGAGATCAAAACCAACTGTGGCTGCACCATCTGTC 351
Qy 430 T 430
Db 352 T 352

RESULT 13
US-09-453-234-41
; Sequence 41, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
; APPLICANT: Buechler, Joe
; APPLICANT: Walkers, Gunars
; APPLICANT: Gray, Jeff
; APPLICANT: Lomborg, Nils
; APPLICANT: Biosite Diagnostics, Inc.

APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIORITY APPLICATION NUMBER: US 60/157,415
PRIORITY FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 41
LENGTH: 678
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(678)
OTHER INFORMATION: M1-5L
US-09-453-234-41

Query Match 33.3%; Score 305.8; DB 11; Length 678;
Best Local Similarity 92.8%; Pred. No. 4.9e-83;
Matches 335; Conservative 0; Mismatches 17; Indels 9; Gaps 1;

QY 70 GATATGTGTGAACGAGTCTCCAGGCACTCTCTTTGCTCCAGGGGAAAGCCACC 129
DB 1 GAAATAGTATGACGAGTCTCCAGGCACTCTCTTTGCTCCAGGGGAAAGCCACC 60
QY 130 CTCTCTGCAAGGCGCAGTCAAGGTGTTAGTACGAGCTAGCTGTTACGACAGAA 189
DB 61 CTCTCTGCAAGGCGCAGTCAAGGTGTTAGTACGAGCTAGCTGTTACGACAGAA 120
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCAGGGGCACTGGCATGCCA 249
DB 121 CTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCAGGGGCACTGGCATGCCA 180
QY 250 GACAGGTTCAAGTGGCAGTGGGTCCGGGACAGACTTCACTTCAACATCACTGAG 309
DB 181 GACAGGTTCAAGTGGCAGTGGGTCCGGGACAGACTTCACTTCAACATCACTGAG 240
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGCATGATGTTAGTACCTCAGACCTCAG 369
DB 241 CCTGAAGATTTTGCAGTGTATTACTGTGACAGCATGATGTTAGTACCTCAGACCTCAG 291
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTC 429
DB 292 TTCACCTTTGGCGGAGGAGCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTC 351
QY 430 T 430
DB 352 T 352

RESULT 14

US-09-453-234-71
Sequence 71, Application US/09453234
Publication No. US20030091995A1
GENERAL INFORMATION:
APPLICANT: Buechler, Joe
APPLICANT: Valikis, Gunarab
APPLICANT: Gray, Jeff
APPLICANT: Lomborg, M118
APPLICANT: Biosite Diagnostics, Inc.
APPLICANT: Genpharm International
TITLE OF INVENTION: Human Antibodies
FILE REFERENCE: 020015-000110US
CURRENT APPLICATION NUMBER: US/09/453,234
CURRENT FILING DATE: 1999-12-01
PRIORITY APPLICATION NUMBER: US 60/157,415
PRIORITY FILING DATE: 1999-10-02
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 71
LENGTH: 678

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(678)
OTHER INFORMATION: M2-11L
US-09-453-234-71

Query Match 33.3%; Score 305.8; DB 11; Length 678;
Best Local Similarity 92.8%; Pred. No. 4.9e-83;
Matches 335; Conservative 0; Mismatches 17; Indels 9; Gaps 1;

QY 70 GATATGTGTGAACGAGTCTCCAGGCACTCTCTTTGCTCCAGGGGAAAGCCACC 129
DB 1 GAAATAGTATGACGAGTCTCCAGGCACTCTCTTTGCTCCAGGGGAAAGCCACC 60
QY 130 CTCTCTGCAAGGCGCAGTCAAGGTGTTAGTACGAGCTAGCTGTTACGACAGAA 189
DB 61 CTCTCTGCAAGGCGCAGTCAAGGTGTTAGTACGAGCTAGCTGTTACGACAGAA 120
QY 190 CCTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCAGGGGCACTGGCATGCCA 249
DB 121 CTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCAGGGGCACTGGCATGCCA 180
QY 250 GACAGGTTCAAGTGGCAGTGGGTCCGGGACAGACTTCACTTCAACATCACTGAG 309
DB 181 GACAGGTTCAAGTGGCAGTGGGTCCGGGACAGACTTCACTTCAACATCACTGAG 240
QY 310 CCTGAAGATTTTGCAGTGTATTACTGTGACAGCATGATGTTAGTACCTCAGACCTCAG 369
DB 241 CCTGAAGATTTTGCAGTGTATTACTGTGACAGCATGATGTTAGTACCTCAGACCTCAG 291
QY 370 ATCACTTTGGCGGAGGAGCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTC 429
DB 292 TTCACCTTTGGCGGAGGAGCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTC 351
QY 430 T 430
DB 352 T 352

RESULT 15

US-10-041-860-59
Sequence 59, Application US/10041860
Publication No. US20030157109A1
GENERAL INFORMATION:
APPLICANT: Corvatan, Jose R.F.
APPLICANT: Jia, Xiao-Chi
APPLICANT: Feng, Xiao
APPLICANT: Yang, Xiao-Dong
APPLICANT: Chen, Francine
APPLICANT: Gazic, Gadi
APPLICANT: Weber, Richard
APPLICANT: Bezebe, Binyam
TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGF AND USES
FILE REFERENCE: ARGENIX 051A
CURRENT APPLICATION NUMBER: US/10/041,860
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 377
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 59
LENGTH: 379
TYPE: DNA
ORGANISM: homo sapiens
US-10-041-860-59

Query Match 33.1%; Score 303.8; DB 12; Length 379;
Best Local Similarity 89.4%; Pred. No. 1.6e-82;
Matches 339; Conservative 0; Mismatches 37; Indels 3; Gaps 1;

QY 478 CAGTGCACCTGATGAGTCTGGGGAGGCGTGTCTCAGCTGGAGGTCCTGAGACTC 537
|||||

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Db      1 CAGGTGCACTGTGGAGTCCGGGGGAGGCGGTGTCAGCCTGGGAAATCCCTGAGACTC 60
QY      538 TCCTGTGAGGCTCTGATTCCTTCAGAACTTTGCTATGCACTGGTCGGCCAGGCT 597
Db      61 TCCTGTGAGGCTCTGATTCCTTCAGAACTTTGCTATGCACTGGTCGGCCAGGCT 120
QY      598 CTAGGCAGGGGCTGAGTGGGTGGCAGTTATATATGATGGAAGCACTAAATACTAC 657
Db      121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATATGATGGAAGCACTAAATACTAT 180
QY      658 GCAGACTCCGTGAAGGGCCGATTCCACATCTCCAGAGACACTTCCAGAGACACGGTGAT 717
Db      181 GCAGACTCCGTGAAGGGCCGATTCCACATCTCCAGAGACACTTCCAGAGACACGGTGAT 240
QY      718 CTAAATATGAACAGCTTGAGAACTGAGAGACAGGCTGTCTATTACTGTGCGAGATCAG 777
Db      241 CTGCAATATGAACAGCTTGAGAGCCGAGAGACAGGCTGTGTATTACTGTGCGAGATCAA 300
QY      778 AG---CCTGTGGGTGACTATGACCACTACTACGTTTGGACGTCTGGGGCAAGGACC 834
Db      301 GGATACAGATATGCTGTTACTACTACGACTACGATATGACGTCCTGGGGCCAAAGGACC 360
QY      835 ACGGTACCGTCTCTCTCAG 853
Db      361 ACGGTACCGTCTCTCTCAG 379
```

Search completed: September 17, 2003, 05:31:54
Job time : 876 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 02:57:14 ; Search time 1933 Seconds
(without alignments)
11542.426 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918
Sequence: 1 GAATTCATGAAAAAACCGC.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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28: gb_esc1.*
29: gb_esc2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	317.6	34.6	584	10	BF664453	BF664453 602146204
2	314.8	34.3	516	9	AM401728	AM401728 UI-HF-BKO
3	313.4	34.1	536	9	AM402624	AM402624 UI-HF-BKO
4	311	33.9	881	13	BQ709375	BQ709375 AGENCOURT

Result No.	Score	Match	Length	DB	ID	Description
5	310.6	33.8	979	13	BQ709399	BQ709399 AGENCOURT
6	309	33.7	424	10	BF874079	BF874079 IL3-ET011
7	308.6	33.6	566	9	AM405972	AM405972 UI-HF-BLO
8	308	33.6	745	12	B1759245	B1759245 603042678
9	307.8	33.5	433	9	AV647117	AV647117 AV647117
10	307.8	33.5	440	9	AV647111	AV647111 AV647111
11	307.8	33.5	504	9	AM405787	AM405787 UI-HF-BLO
12	307.8	33.5	734	10	BG686748	BG686748 602650717
13	307.8	33.5	793	9	AV646708	AV646708 AV646708
14	307.8	33.5	926	13	BQ706634	BQ706634 AGENCOURT
15	307.8	33.5	998	13	BQ709245	BQ709245 AGENCOURT
16	307.2	33.4	801	13	BK399298	BK399298 BK399298
17	306.2	33.4	518	9	AM406576	AM406576 UI-HF-BLO
18	306.2	33.4	862	10	BG758749	BG758749 602713108
19	306.2	33.4	1014	12	BM918339	BM918339 AGENCOURT
20	306	33.3	456	9	AM406451	AM406451 UI-HF-BLO
21	305.8	33.3	472	9	AM405697	AM405697 UI-HF-BLO
22	305.8	33.3	603	9	AM404910	AM404910 UI-HF-BLO
23	304.6	33.2	933	13	BQ711272	BQ711272 AGENCOURT
24	304.2	33.1	526	13	BQ331002	BQ331002 QV3-ET019
25	303.8	33.1	1069	12	BM919414	BM919414 AGENCOURT
26	303.4	33.1	1153	10	BF663521	BF663521 602144686
27	303	33.0	441	10	BF914735	BF914735 IL3-UT011
28	303	33.0	441	10	BF914740	BF914740 IL3-UT011
29	303	33.0	488	12	BM830796	BM830796 K-EST0104
30	303	33.0	504	10	BF917294	BF917294 IL3-UT011
31	303	33.0	544	9	AM405216	AM405216 UI-HF-BLO
32	303	33.0	644	9	AM405817	AM405817 UI-HF-BLO
33	303	33.0	859	13	BK368110	BK368110 BK368110
34	303	33.0	923	13	BQ711051	BQ711051 AGENCOURT
35	303	33.0	974	13	BQ707037	BQ707037 AGENCOURT
36	302.6	33.0	489	9	AM406488	AM406488 UI-HF-BLO
37	302.4	32.9	1201	13	BK357917	BK357917 BK357917
38	301.8	32.8	976	12	BM914525	BM914525 AGENCOURT
39	301.4	32.8	978	13	BQ707988	BQ707988 AGENCOURT
40	301	32.8	786	14	CB956522	CB956522 AGENCOURT
41	301	32.8	917	13	BQ711815	BQ711815 AGENCOURT
42	300.6	32.7	718	14	CB957976	CB957976 AGENCOURT
43	299.8	32.7	707	10	BG685522	BG685522 602637389
44	299.8	32.7	786	14	CB957311	CB957311 AGENCOURT
45	299.8	32.7	840	10	BG685798	BG685798 602637907

ALIGNMENTS

RESULT 1
BF664453
LOCUS 602146204F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4309680 5',
DEFINITION mRNA sequence.
ACCESSION BF664453.1 GI:11938258
VERSION BF664453.1
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished
JOURNAL
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-rtmail.nih.gov
Tissue Procurement: Louis M. Staute, M.D., Ph.D.
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution/ILNL at:
found through the I.M.A.G.E. Consortium/ILNL at:
http://image.llnl.gov
Plate: L1CML183 row: h column: 01
High quality sequence stop: 584.

FEATURES

Location/Qualifiers
1. 584

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4309680"
/tissue_type="Primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."

BASE COUNT 139 a 168 c 153 g 124 t

ORIGIN

Query Match 34.6%; Score 317.6; DB 10; Length 584;
Best Local Similarity 87.3%; Pred. No. 2.7e-71;
Matches 363; Conservative 0; Mismatches 44; Indels 9; Gaps 1;

15 AACCGTATCGCGCATCGAGTTCAGTCTGTTGGCTACCGTGGCAGGCCGATAT 74
17 AAACCCAGCGCGAGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 76
75 TGTGTGAGCGCAGTCTTCAGGACCCCTGTTTGTCTCCAGGGGAAAGCCCTCTC 134
77 TGTGTGAGCGCAGTCTTCAGGACCCCTGTTTGTCTCCAGGGGAAAGCCCTCTC 136
135 CTGCAAGGCGCAGTCTTCAGGACCCCTGTTTGTCTCCAGGGGAAAGCCCTCTC 194
137 CTGCAAGGCGCAGTCTTCAGGACCCCTGTTTGTCTCCAGGGGAAAGCCCTCTC 196
195 CCAAGGCTCCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 254
197 CCAAGGCTCCAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 256
255 GTTCAGTGGCAGTGGTCTCGGGACAGCTTCACTCTCCATCCATCAGTGAAGCTCTGA 314
257 GTTCAGTGGCAGTGGTCTCGGGACAGCTTCACTCTCCATCCATCAGTGAAGCTCTGA 316
315 AGATTTTGCAGTGTATTAATCTGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 374
317 AGATTTTGCAGTGTATTAATCTGTGAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAG 367
375 TTTCCGCGGAGGAGCCAAAGGTGAGATCAACGAACTGTGGCTGCACCATCTGTCT 430
368 TTTCCGCGGAGGAGCCAAAGGTGAGATCAACGAACTGTGGCTGCACCATCTGTCT 423

RESULT 2
AM401728 516 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
IMAGE:3053711 5', mRNA sequence.
AM401728
AM401728.1 GI:6920414
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Straudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:
www-bio.liml.gov/biopr/image/image.html
Seq primer: M13 forward

FEATURES

Location/Qualifiers
1. 516

source
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053711"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pT73-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Straudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 112 a 132 c 150 g 122 t

ORIGIN

Query Match 34.3%; Score 314.8; DB 9; Length 516;
Best Local Similarity 85.8%; Pred. No. 1.3e-70;
Matches 362; Conservative 0; Mismatches 57; Indels 3; Gaps 1;

440 GCGGTCCGAGGTGGTGTGATCAGTGGAGTGGCTCCAGGTGCGAGTGGTGGAGTGG 499
93 GGGTTTCTCTGTTGCTCTTTTAAGAGTGTCCAGTGTACAGGTGGTGGAGTGG 152
500 GGGAGGCGGTGTGTCAGGCTGGAGGCTCCCTGAGACTCTCTGTCAGCTCTGATTC 559
153 GGGAGGCGGTGTGTCAGGCTGGAGGCTCCCTGAGACTCTCTGTCAGCTCTGATTC 212
560 CCTTCAGAAAGCTTGTCTATGACACTGGGTCCGCCAGCTCTAGGCAAGGGCTGGAGTGG 619
213 CCTTCAGTGTGTATGTATGACACTGGGTCCGCCAGCTCTAGGCAAGGGCTGGAGTGG 272
620 TGGCAATTATATATATATATATATATATATATATATATATATATATATATATATATAT 679
273 TGGCAATTATATATATATATATATATATATATATATATATATATATATATATATATAT 332
680 TCACCATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTAAATGAACAGCTGAGAA 739
333 TCACCATCTCCAGAGACACTTCCAGAGACAGGCTGTATCTGCAATAGAACAGCTGAGAA 392
740 CTGAGGACACGGCTGTCTTATCTGTGCGAGAGATGAGGCC--TGTGGGTGACTATG 796
393 CTGAGGACACGGCTGTCTTATCTGTGCGAGAGAGCCCTGTGCTCTTACGGTGAATTCACCT 452
797 ACCACTACTACGGTTTGAAGTCTGGGGGAAAGGAGCAAGGTCACCGTCTCTCAGGAT 856
453 ACTACTACTACGGTTTGAAGTCTGGGGGAAAGGAGCAAGGTCACCGTCTCTTTCAGCTT 512

RESULT 3
AM402624 536 bp mRNA linear EST 16-FEB-2000
LOCUS
DEFINITION
IMAGE:3053559 5', mRNA sequence.
AM402624
AM402624.1 GI:6921329
VERSION
KEYWORDS
SOURCE
Homo sapiens (human)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
NIH-MGC http://mgs.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
Contact: Robert Strausberg, Ph.D.
Email: cgapsb-remail.nih.gov
Eco RI site shown at the beginning of the sequence.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 536)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbp/image/image.html
Seq primer: M13 Forward

FEATURES
source
1..536
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:305359"
/issue_type="lymph"
/cell_line="germinal center B cells"
/lab_host="DH10B (LT1)"
/clone_1ib="NIH MGC 36"
/note="Vector: pT7-3-Pac; Site_1: NotI; Site_2: Eco RI;
constructed from size fractionated cytoplasmic mRNA
(0.5-1.5kb). Directionally cloned. Cells provided by Louis
M. Staudt, Ph.D. Library preparation by Maria de Fatima
Bonaldi, Ph.D. and M. Bento Soares, Ph.D."

BASE COUNT 113 a 141 c 160 g 122 t

ORIGIN
Query Match 34.1%; Score 313.4; DB 9; Length 536;
Best Local Similarity 85.9%; Pred. No. 3.2e-70;
Matches 360; Conservative 0; Mismatches 56; Indels 3; Gaps 1;

QY 440 GGGGTTCCGAGAGTGTGATGATGAGTGGCTCCAGGTCAGCTGTGGAGTCTG 499
DB 57 GGGGTTTCTCGTGTCTTTAAGAGGTGTCCAGTGTCAAGTGCAGCTGTGGAGTCTG 116
QY 500 GGGGAGGCGTGGTCCAGCTGGAGAGTCCCTGAGACTCTGTGAGCTCTGATTC 559
DB 117 GGGGAGGCGTGGTCCAGCTGGAGAGTCCCTGAGACTCTGTGAGCTCTGATTC 176
QY 560 CCTTGAGAGCTTTGCTATGCACTGGGTCCGAGGCTCTAGGCAAGGGCTGGAGTGG 619
DB 177 CCTTGAGAGCTTTGCTATGCACTGGGTCCGAGGCTCTAGGCAAGGGCTGGAGTGG 236
QY 620 TGGCAGTTATCATATGATGAGACATAAATCTAGCAGACTCCGTGAAGGCGAT 679
DB 237 TGGCAGTTATCATATGATGAGACATAAATCTAGCAGACTCCGTGAAGGCGAT 296
QY 680 TCACCATCTCCAGAGCACTCCAGAGACAGCGTGTATTAATAATGAACAGCTGAGAA 739
DB 297 TCACCATCTCCAGAGCACTCCAGAGACAGCGTGTATGCAAAAGAACAGCTGAGAA 356
QY 740 CTGAGAGCAAGGCTGTCTATTAATGCTGAGAGATGAGAGCTGTGGTGAATGACC 799
DB 357 CTGAGAGCAAGGCTGTCTATTAATGCTGAGAGATGAGAGCTGTGGTGAATGACC 413
QY 800 ACTACTACGCTTGGAGCGTGTGGGCAAGGAGCAAGGCTACCGTCTCTAGGCTCC 858
DB 414 ACTACTACGCTTGGAGCGTGTGGGCAAGGAGCAAGGCTACCGTCTCTAGGCTCC 472

RESULT 4
BQ709375 LOCUS BQ709375 881 bp mRNA linear EST 16-JUL-2002

DEFINITION AGENCOURT_7977299 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215729
5', mRNA sequence.
ACCESSION BQ709375
VERSION BQ709375.1 GI:21848274
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 881)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2385 row: b column: 18
High quality sequence stop: 700.

FEATURES
source
1..881
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6215729"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NIH MGC 113"
/note="Organ: spleen; Vector: pOT7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."

BASE COUNT 198 a 275 c 218 g 188 t 2 others

ORIGIN
Query Match 33.9%; Score 311; DB 13; Length 881;
Best Local Similarity 93.9%; Pred. No. 1.7e-69;
Matches 339; Conservative 0; Mismatches 10; Indels 12; Gaps 1;

QY 70 GATATGTTGTTGACGAGCTCTCCAGGCAACCTGTCTTGTCTCCAGGGGAAAGCCACC 129
DB 70 GATATGTTGTTGACGAGCTCTCCAGGCAACCTGTCTTGTCTCCAGGGGAAAGCCACC 129
QY 130 CTCTCTCCAGGCGCAGTCAGAGTGTAGTACACTTATGCTGTGATCCAGAGAA 189
DB 130 CTCTCTCCAGGCGCAGTCAGAGTGTAGTACACTTATGCTGTGATCCAGAGAA 189
QY 190 CTGAGCAGAGCTCCAGGCTCTCATATGATGATGATGATGATGATGATGATGATGAT 249
DB 190 CTGAGCAGAGCTCCAGGCTCTCATATGATGATGATGATGATGATGATGATGATGAT 249
QY 250 GACAGGTTCAAGTGGAGTGGGTCTGGAGACAGCTTCACTCATCAGCAGAGCTGGAG 309
DB 250 GACAGGTTCAAGTGGAGTGGGTCTGGAGACAGCTTCACTCATCAGCAGAGCTGGAG 309
QY 310 CCTGAAAGTTTGGAGTGTATTAATGCTGAGAGTGTAGTGTAGTGTAGTGTAGTGTAG 369
DB 310 CCTGAAAGTTTGGAGTGTATTAATGCTGAGAGTGTAGTGTAGTGTAGTGTAGTGTAG 369
QY 370 ATCACTTTCGAGAGGAGCACAAGGTGAGATCAAAAGCACTGTGGCTGACCATCTGTC 429
DB 358 GTCACTTTCGAGAGGAGCACAAGGTGAGATCAAAAGCACTGTGGCTGACCATCTGTC 417

430 T 430

Db 418 T 418

RESULT 5
BQ709399

LOCUS
DEFINITION
AGENCOURT 7972270 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6215847
5', mRNA sequence.

ACCESSION
BQ709399

VERSION
BQ709399.1 GI:21848298

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 979)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE
Unpublished

AUTHORS
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov

COMMENT
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.lnl.gov>
Plate: L10M2385 row: 9 column: 16
High quality sequence stop: 401.
Location/Qualifiers

FEATURES

source

1..979

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6215847"

/lab_host="DH10B (phage-resistant)"

/clone_1ib="NIH MGC 113"

/note="Organ: spleen; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
Laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library"

BASE COUNT 204 a 295 c 283 g 197 t

ORIGIN

Query Match 33.8%; Score 310.6; DB 13; Length 979;
Best Local Similarity 93.4%; Pred. No. 2.2e-69;
Matches 338; Conservative 0; Mismatches 14; Indels 9; Gaps 1;

QY 70 GATTGTGTTGACGCGCTCCAGGACCCCTGTTGTCCTCCAGGGGAAAGCCACC 129

Db 80 GAAATTTGTTGACGCGCTCCAGGACCCCTGTTGTCCTCCAGGAGAGAGCCACC 139

QY 130 CTCTCTGCGAGGGGCACTCAGAGGTAGTACGACTTACCTGCTGCTACCGAGGAA 189

Db 140 CTCTCTGCGAGGGGCACTCAGAGGTAGTACGACTTACCTGCTGCTACCGAGGAA 199

QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCCACTGGCATGCCA 249

Db 200 CTTGGCCAGGCTCCAGGCTCTCATCTATGTCATCCACGAGGCCACTGGCATGCCA 259

QY 250 GACAGGTTAGTGGCACTGGGTCCGGAGCAGACTTCACTCAACCATCAGTAGAG 309

Db 260 GACAGGTTAGTGGCACTGGGTCCGGAGCAGACTTCACTCAACCATCAGTAGAG 319

QY 310 CCTGAAGATTTCAGTGTATTAAGTACAGAGATGATGCTCAGTCAAGACCTGAG 369

Db 320 CCTGAAGATTTCAGTGTATTAAGTACAGAGATGATGCTCAGTCAAGACCTGAG 370

QY 370 ATCACTTTCGCGGAGGACCAAGTGGAGATCAACGAACTGTGCTGCACCATCTGC 429

Db 371 ATCACTTTCGCGGAGGACCAAGTGGAGATCAACGAACTGTGCTGCACCATCTGC 430

QY 430 T 430

Db 431 T 431

RESULT 6
BF874079

LOCUS
DEFINITION
IL3-ET0115-071100-302-D08 ET0115 Homo sapiens cDNA, mRNA sequence.

ACCESSION
BF874079

VERSION
BF874079.1 GI:12264209

KEYWORDS
EST.

SOURCE
Homo sapiens (human)

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
20202663

PUBMED
10737800

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?tl=IL3&t2=IL3-ET0115-071100-302-D08&t3=2000-11-07&t4=1>)
Seq primer: puc 18 forward
High quality sequence stop: 392.
Location/Qualifiers

FEATURES

source

1..424

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/dev_stage="Adult"

/clone_1ib="ET0115"

/note="Organ: lung_tumor; Vector: puc18; Site_1: SmaI;
Site_2: SmaI; A mini-library was made by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

BASE COUNT 90 a 127 c 111 g 96 t

ORIGIN

Query Match 33.7%; Score 309; DB 10; Length 424;
Best Local Similarity 93.4%; Pred. No. 3.9e-69;
Matches 337; Conservative 0; Mismatches 15; Indels 9; Gaps 1;

QY 70 GATTGTGTTGACGCGCTCCAGGACCCCTGTTGTCCTCCAGGGGAAAGCCACC 129

Db 61 GAAATTTGTTGACGCGCTCCAGGACCCCTGTTGTCCTCCAGGGGAAAGCCACC 120

QY 130 CTCTCTGCGAGGGGCACTCAGAGGTAGTACGACTTACCTGCTGCTACCGAGGAA 189

Db 121 CTCCTCGACGGCCAGTACAGTGTTCAGCAGCAGCTTACCTTGATCCAGCGAAG 180
 Oy 190 CCTGGCAGAGCTCCAGAGCTCTCATCTATGTGATCCAGAGGCCACTGGCATGCCA 249
 Db 181 CCTGGCAGAGCTCCAGAGCTCTCATCTATGTGATCCAGAGGCCACTGGCATGCCA 240
 Oy 250 GACAGGTTGAGTGGCAGTGGGTCCGGACAGACTTCACTTCACCATCAGTAGACTGGAG 309
 Db 241 GACAGGTTGAGTGGCAGTGGGTCCGGACAGACTTCACTTCACCATCAGTAGAG 300
 Oy 310 CCGAAGATTTTGCAGTGTATTAATGTCAGCAGTGTAGTACCTCAGACCTCAG 369
 Db 301 CCGAAGATTTTGCAGTGTATTAATGTCAGCAGTGTAGTACCTCAGACCTCAG 351
 Oy 370 ATCACTTTGGCGGAGGACCAAGTGTGAGATCAAGAACTGTGGCTGACCATCTGTC 429
 Db 352 CTCACCTTTGGCGGAGGACCAAGTGTGAGATCAAGAACTGTGGCTGACCATCTGTC 411
 Oy 430 T 430
 Db 412 T 412

RESULT 7
 AM405972 566 bp mRNA linear EST 16-FEB-2000
 LOCUS UI-HF-BL0-acv-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
 DEFINITION IMAGE:3060360 5', mRNA sequence.
 ACCESSION AM405972
 VERSION AM405972.1 GI:6925029
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS 1 (baees 1 to 366)
 JOURNAL NIH-MGC http://mgs.nci.nih.gov/.
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 CDNA Library Preparation: M.B. Soares Lab
 CDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 www-bio.llnl.gov/dbtrp/image/image.html
 Seq primer: M13 Forward.

FEATURES

source 1..566
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3060360"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_lib="NIH_MGC_37"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonafide, Ph.D. and M. Bento Soares, Ph.D."
 BASE COUNT 129 a 169 c 145 g 123 t

Query Match 33.6%; Score 308.6; DB 9; Length 566;
 Best Local Similarity 93.1%; Pred. No. 5.6e-69;
 Matches 336; Conservative 0; Mismatches 19; Indels 6; Gaps 1;

Oy 70 GATATTGTGTACGAGCTCTCCAGGACCTGTCTTTGTCTCCAGGGGAAAGACCACC 129
 Db 66 GAAATGTGTACGAGCTCTCCAGGACCTGTCTTTGTCTCCAGGGGAAAGACCACC 125
 Oy 130 CTCTCTGACAGGCCCAATGAGTGTATGATGAGTATTTAGCTGTGATCCAGCGA 189
 Db 126 CTCTCTGACAGGCCCAATGAGTGTATGATGAGTATTTAGCTGTGATCCAGCGA 185
 Oy 190 CCTGGCAGAGCTCCAGAGCTCTCATCTATGTGATCCAGAGGCCACTGGCATGCCA 249
 Db 186 CCTGGCAGAGCTCCAGAGCTCTCATCTATGTGATCCAGAGGCCACTGGCATGCCA 245
 Oy 250 GACAGGTTGAGTGGCAGTGGGTCCGGACAGACTTCACTTCACCATCAGTAGACTGGAG 309
 Db 246 GACAGGTTGAGTGGCAGTGGGTCCGGACAGACTTCACTTCACCATCAGTAGAG 305
 Oy 310 CCGAAGATTTTGCAGTGTATTAATGTCAGCAGTGTAGTACCTCAGACCTCAG 369
 Db 306 CCGAAGATTTTGCAGTGTATTAATGTCAGCAGTGTAGTACCTCAGACCTCAG 359
 Oy 370 ATCACTTTGGCGGAGGACCAAGTGTGAGATCAAGAACTGTGGCTGACCATCTGTC 429
 Db 360 CTCACCTTTGGCGGAGGACCAAGTGTGAGATCAAGAACTGTGGCTGACCATCTGTC 419
 Oy 430 T 430
 Db 420 T 420

RESULT 8
 B1759245 745 bp mRNA linear EST 25-SEP-2001
 LOCUS 603042678F1 NIH_MGC_116 Homo sapiens cDNA clone IMAGE:518910 5',
 DEFINITION mRNA sequence.
 ACCESSION B1759245
 VERSION B1759245.1 GI:15750823
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 AUTHORS 1 (baees 1 to 745)
 JOURNAL NIH-MGC http://mgs.nci.nih.gov/.
 COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: L14M11456 row: 1 column: 19
 High quality sequence stop: 724.

FEATURES

source 1..745
 Location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:518910"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_116"
 /note="Organ: pooled colon, kidney, stomach; Vector:
 pCMV-SpORe; Site 1: NotI; Site 2: EcoRV (destroyed); RNA
 source anonymous pool of 3 colons, age 26 yo male, 49 yo
 female, 71 yo male colon; 46 yo male kidney, and pool of 2
 stomachs, 62 yo male and 70 yo female. Library is
 oligo-dT primed and directionally cloned (EcoRV site is
 destroyed upon cloning). Average insert size 1.4 kb,
 insert size range 1-3 kb. Library is normalized and
 enriched for full-length clones and was constructed by C.

FEATURES

Source

Location/Qualifiers
 1. 440
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GLCAUG10"
 /tissue_type="corresponding non cancerous liver tissue"
 /dev_stage="Adult"
 /lab_host="SOLR"
 /clone_1ib="GLC"
 /note="Vector: pBluescript sk(-); Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 96 a 132 c 116 g 95 t 1 others
 ORIGIN

Query Match 33.5%; Score 307.8; DB 9; Length 440;
 Best Local Similarity 93.4%; Pred. No. 8.1e-69;
 Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATGTGTGACGACGCTTCACGACACCTGTCTTGTCTCCAGGGGAAAGACCAACC 129
 91 GAAATTTGTGTGACGACGCTTCACGACACCTGTCTTGTCTCCAGGGGAAAGACCAACC 150
 130 CTCTCTCGAGGGCCAGTCAAGTGTGTAGTACGACCTTACCTGGTACGACAGAA 189
 151 CTCTCTCGAGGGCCAGTCAAGTGTGTAGTACGACCTTACCTGGTACGACAGAA 210
 190 CCGGCGAGGCTCCAGGCTCTCATATGCTGATCCACAGGGGCCACTGGATGCCA 249
 211 CTGGCCAGGCTCCAGGCTCTCATATGCTGATCCACAGGGGCCACTGGATGCCA 270
 250 GACAGTTCACTGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 309
 271 GACAGTTCACTGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 330
 310 CCTGAAGTTTTCAGTGTATTAATCTGACGACGATGTAGTACCTCAGACACTCAG 369
 331 CCTGAAGTTTTCAGTGTATTAATCTGACGACGATGTAGTACCTCAGACACTCAG 379
 370 ATCACTTTCGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTAGTACCTCAGTGTG 429
 380 -TCACTTTCGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTAGTACCTCAGTGTG 438
 430 T 430
 439 T 439

RESULT 11
 AM405787 504 bp mRNA linear EST 16-FEB-2000
 LOCUS .
 DEFINITION UI-HF-BL0-abp-e-02-0-UI-r1 NIH_MGC_37 Homo sapiens cDNA clone
 IMAGE:3057482 5', mRNA sequence.

ACCESSION AM405787
 VERSION AM405787.1 GI:6924844
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Eco RI site shown at the beginning of the sequence.
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
 cDNA Library Preparation: M.B. Soares Lab
 cDNA Library Arrayed by: M.B. Soares Lab
 DNA Sequencing by: M.B. Soares Lab
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:

FEATURES

Source

Location/Qualifiers
 1. 504
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:3057482"
 /tissue_type="lymph"
 /cell_type="germinal center B cells"
 /cell_line="MGC85"
 /lab_host="DH10B (LTI)"
 /clone_1ib="NIH_MGC_37"
 /note="Vector: pT73-Pac; Site 1: NotI; Site 2: Eco RI;
 Constructed from size fractionated cytoplasmic mRNA
 (1.5-2.5kb). Directionally cloned. Cells provided by Louis
 M. Staudt, Ph.D. Library preparation by Maria de Fatima
 Bonaldo, Ph.D. and W. Bento Soares, Ph.D."

BASE COUNT 117 a 147 c 127 g 113 t
 ORIGIN

Query Match 33.5%; Score 307.8; DB 9; Length 504;
 Best Local Similarity 93.4%; Pred. No. 8.6e-69;
 Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

70 GATATGTGTGACGACGCTTCACGACACCTGTCTTGTCTCCAGGGGAAAGACCAACC 129
 74 GAAATTTGTGTGACGACGCTTCACGACACCTGTCTTGTCTCCAGGGGAAAGACCAACC 133
 130 CTCTCTCGAGGGCCAGTCAAGTGTGTAGTACGACCTTACCTGGTACGACAGAA 189
 134 CTCTCTCGAGGGCCAGTCAAGTGTGTAGTACGACCTTACCTGGTACGACAGAA 193
 190 CCGGCGAGGCTCCAGGCTCTCATATGCTGATCCACAGGGGCCACTGGATGCCA 249
 194 CTGGCCAGGCTCCAGGCTCTCATATGCTGATCCACAGGGGCCACTGGATGCCA 253
 250 GACAGTTCACTGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 309
 254 GACAGTTCACTGAGTGGGTCGGGACAGACTTCACTTCACCATCAGTACGATGGAG 313
 310 CCTGAAGTTTTCAGTGTATTAATCTGACGACGATGTAGTACCTCAGACACTCAG 369
 314 CCTGAAGTTTTCAGTGTATTAATCTGACGACGATGTAGTACCTCAGACACTCAG 364
 370 ATCACTTTCGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTAGTACCTCAGTGTG 429
 365 --ACGTTTCGGCGGAGGACCAAGGTGAGATCAAGCAAGTGTAGTACCTCAGTGTG 421
 430 T 430
 422 T 422

RESULT 12
 BG686748 734 bp mRNA linear EST 01-MAY-2001
 LOCUS .
 DEFINITION 602650717P1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763021 5',
 mRNA sequence.

ACCESSION BG686748
 VERSION BG686748.1 GI:13918145
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished

CONTACT: Robert Strausberg, Ph.D.
 Email: cga@bbs-remail.nih.gov
 Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

VERSION B0706634.1 GI:21845533
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 926)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strusberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LCM2383 row: h column: 07
 High quality sequence stop: 536.
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6215094"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC library."

BASE COUNT 213 a 278 c 239 g 196 t
 ORIGIN
 Query Match 33.5%; Score 307.8; DB 13; Length 926;
 Best Local Similarity 93.4%; Pred. No. 1.1e-68;
 Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTGTTGACGACGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGCCACC 129
 DB 67 GAAATTGTTGACGACGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGCCACC 126
 QY 130 CTCTCTCAGGGGCACTAGAGTTAGTAGCAGCTTACTTACCTGTGACGAGAAA 189
 DB 127 CTCTCTCAGGGGCACTAGAGTTAGTAGCAGCTTACTTACCTGTGACGAGAAA 186
 QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 249
 DB 187 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 246
 QY 250 GACAGTTCACTGAGGAGGTCGGGACAGACTTCACTTCACATCAGTAGAGCTGGAG 309
 DB 247 GACAGTTCACTGAGGAGGTCGGGACAGACTTCACTTCACATCAGTAGAGCTGGAG 306
 QY 310 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTAGTAGCTCACTCAGACCTCGAG 369
 DB 307 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTAGTAGCTCACTCAGACCTCGAG 364
 QY 370 ATCACTTTGGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGCACCATCTGTC 429
 DB 355 CTCACCTTTGGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGCACCATCTGTC 414
 QY 430 T 430
 DB 415 T 415

RESULT 15
 B0709245 998 bp mRNA linear EST 16-JUL-2002
 LOCUS AGNCOURT_7975569 NIH_MGC_113 Homo sapiens CDNA clone IMAGE:6214925
 DEFINITION 5' mRNA sequence.
 ACCESSION B0709245
 VERSION B0709245
 KEYWORDS B0709245.1 GI:21848144
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 REFERENCE 1 (bases 1 to 998)
 AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished
 COMMENT Contact: Robert Strusberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Mark Watson
 CDNA Library Preparation: Rubin Laboratory
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
 Plate: LCM2383 row: a column: 06
 High quality sequence stop: 500.
 Location/Qualifiers
 1..998
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6214925"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_113"
 /note="Organ: spleen; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; CDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH MGC library."

BASE COUNT 240 a 290 c 265 g 203 t
 ORIGIN
 Query Match 33.5%; Score 307.8; DB 13; Length 998;
 Best Local Similarity 93.4%; Pred. No. 1.2e-68;
 Matches 337; Conservative 0; Mismatches 12; Indels 12; Gaps 1;

QY 70 GATATTGTTGACGACGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGCCACC 129
 DB 66 GAAATTGTTGACGACGCTCCAGGACCCCTGTCTTGTCTCCAGGGGAAGCCACC 125
 QY 130 CTCTCTCAGGGGCACTAGAGTTAGTAGCAGCTTACTTACCTGTGACGAGAAA 189
 DB 126 CTCTCTCAGGGGCACTAGAGTTAGTAGCAGCTTACTTACCTGTGACGAGAAA 185
 QY 190 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 249
 DB 186 CTTGGCCAGGCTCCAGGCTCTCATCTATGTTGATCCAGGAGGCACTGGCATGCCA 245
 QY 250 GACAGTTCACTGAGGAGGTCGGGACAGACTTCACTTCACATCAGTAGAGCTGGAG 309
 DB 246 GACAGTTCACTGAGGAGGTCGGGACAGACTTCACTTCACATCAGTAGAGCTGGAG 305
 QY 310 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTAGTAGCTCACTCAGACCTCGAG 369
 DB 306 CTTGAAGATTTTGCAGTGTATTACTGTACAGAGTAGTAGCTCACTCAGACCTCGAG 363
 QY 370 ATCACTTTGGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGCACCATCTGTC 429
 DB 354 CTCACCTTTGGGCGAGGACCAAGGTGAGATCAAGCACTGTGGCTGCACCATCTGTC 413

Qy	430 T 430
Db	414 T 414

Search completed: September 17, 2003, 04:21:49
Job time : 1938 secs

Yaen, C.
09/19/04 164 Page 1
08/16/57449
Seq. ID 13 w/ notes

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Comugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 03:02:49 ; Search time 2893 Seconds
(without alignments)
10523.453 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918
Sequence: 1 GAATTCATGAAAAAACC...ATCACCATTAAGTGAAGCTT 918

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 3353688 seqs, 1658189874 residues

Total number of hits satisfying chosen parameters: 66727376

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 90: /cgn2_6/ptodata/2/pna/US6047_COMB.seq.*
- 91: /cgn2_6/ptodata/2/pna/US6048_COMB.seq.*
- 92: /cgn2_6/ptodata/2/pna/US6049_COMB.seq.*
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- 99: /cgn2_6/ptodata/2/pna/US6056_COMB.seq.*
- 100: /cgn2_6/ptodata/2/pna/US6057_COMB.seq.*
- 101: /cgn2_6/ptodata/2/pna/US6058_COMB.seq.*
- 102: /cgn2_6/ptodata/2/pna/US6059_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	11	US-08-657-449-13
2	918	100.0	918	30	US-09-697-561-13
3	918	100.0	918	30	US-09-697-561A-13
4	918	100.0	918	33	US-09-782-397-13

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5 918 100.0 918 33 US-09-782-397A-13 Sequence 13, Appl
7 918 100.0 918 33 US-09-782-397B-13 Sequence 13, Appl
8 916.4 99.8 918 11 US-08-657-449-15 Sequence 15, Appl
9 916.4 99.8 918 30 US-09-697-561-15 Sequence 15, Appl
10 916.4 99.8 918 30 US-09-697-561A-15 Sequence 15, Appl
11 916.4 99.8 918 33 US-09-782-397-15 Sequence 15, Appl
12 916.4 99.8 918 33 US-09-782-397A-15 Sequence 15, Appl
13 916.4 99.8 918 33 US-09-782-397B-15 Sequence 15, Appl
14 916.4 99.8 918 33 US-09-782-397C-15 Sequence 15, Appl
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16 799.6 87.1 867 30 US-09-697-561-16 Sequence 16, Appl
17 799.6 87.1 867 30 US-09-697-561A-16 Sequence 16, Appl
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20 799.6 87.1 867 33 US-09-782-397B-16 Sequence 16, Appl
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29 445 48.5 1630 32 US-09-744-625A-36 Sequence 36, Appl
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32 395.2 43.1 840 2 PCT-US03-10865-20 Sequence 20, Appl
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37 361 39.3 450 33 US-09-782-397-6 Sequence 6, Appl
38 361 39.3 450 33 US-09-782-397A-6 Sequence 6, Appl
39 361 39.3 450 33 US-09-782-397B-6 Sequence 6, Appl
40 361 39.3 450 33 US-09-782-397C-6 Sequence 6, Appl
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44 359.4 39.2 450 33 US-09-782-397-4 Sequence 4, Appl
45 359.4 39.2 450 33 US-09-782-397A-4 Sequence 4, Appl

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ALIGNMENTS

RESULT 1
US-08-657-449-13
Sequence 13, Application US/08657449

GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

APPLICANT: Malt, Michael K.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT

TITLE OF INVENTION: SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/657,449

FILING DATE:

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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..306, 913..918)
US-08-657-449-13

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Query Match 100.0%; Score 918; DB 11; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.5e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-697-561-13
; Sequence 13, Application US/09697561
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maiti, Pradip K.
; KAPLAN, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/697,561
; FILING DATE: 26-Oct-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,124
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Leinhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..906, 913..918)
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-697-561-13

Query Match 100.0%; Score 918; DB 30; Length 918;
Best Local Similarity 100.0%; Pred. No. 2,5e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 3
US-09-697-561A-13
; Sequence 13, Application US/09697561A
; GENERAL INFORMATION:
; APPLICANT: Viventia Biotech Inc.
; APPLICANT: Dan, Michael D.
; APPLICANT: Maiti, Pradip K.
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: Antigen Binding Fragments that Specifically Detect Cancer Cells,
; Nucleotides Encoding the fragments...


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Db      241 GCGATCCAGACAGTTCAGTGGGTCGCGGACAGACTTCACTCTCAGCATCAGT 300
Qy      301 AGACTGAGCCTGGAAGATTTTGCAGTGTATTACTGTACAGATGATGGTACCTCAG 360
Db      301 AGACTGAGCCTGGAAGATTTTGCAGTGTATTACTGTACAGATGATGGTACCTCAG 360
Qy      361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAGAACTGTGCTGCA 420
Db      361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAGAACTGTGCTGCA 420
Qy      421 CCATCTGTCTCTGGCGGTCGCGGTCGCGAGTGTGATCAGTGTGAGGTGCTCCAG 480
Db      421 CCATCTGTCTCTGGCGGTCGCGGTCGCGAGTGTGATCAGTGTGAGGTGCTCCAG 480
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Db      781 CTGTTGGGTGACTATGACCACTACGCTTTGGAAGTCTGGGGCAAGGGACCAAGGTC 840
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Db      841 ACCGTCCTCTCAGAGATCCGAAACAAAATGATCAGGAGAGATCTGAACCATCAGAT 900
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Db      901 CACCATTTAGTGAAGCTT 918

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RESULT 5
US-09-782-397A-13

; Sequence 13, Application US/09782397A

; GENERAL INFORMATION:

; APPLICANT: Dan, Michael D.

; Maitl, Pradip K.

; Kaplan, Howard A.

; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H11, THAT

; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE

; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

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; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster LLP
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/782,397A
; FILING DATE: 13-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/862,124
; FILING DATE: 22-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Lehnhardt, Susan K.
; REGISTRATION NUMBER: 33,943
; REFERENCE/DOCKET NUMBER: 31608-20001.20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 813-5600
; TELEFAX: (650) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 918 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(1..906, 913..918)
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-782-397A-13

Query Match      100.0%; Score 918; DB 33; Length 918;
Best Local Similarity 100.0%; Pred. No. 2.5e-225;
Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GAATTCATGAAAAAACCGCTATCGGATCGCAGTTGCATGCGTGGTTCCGTACCGTT 60
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Db      121 AGAGCCACCTCTCTGCGAGGGCCAGTCAAGTGTGTTAGTAGCAGTACTTACCTGGTAC 180
Qy      181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCCATCTATAGTGTGATCCAGGAGCAGT 240
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Qy      301 AGACTGAGCCTGGAAGATTTTGCAGTGTATTACTGTACAGATGATGGTACCTCAG 360
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Qy      361 ACACCTCAGATCACTTTCCGCGGAGGACCAAGTGTGATCAAGAACTGTGCTGCA 420
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OY	421	CCATCTGATCTCGGCGGTGCGGTTCCGGAGGCGTGGAAACAGTGGAGGTGCTCCAG	480
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Db	601	GGCAAGG3GCTG3AGTGGGTGCGATTTATATCATATGATGAAAGCATAAATCTACGCA	660
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Db	661	GACTCCGTAAAGGGCCGATTCAACCATCTCCAGAGACACTTCCAAAGAACACGGTGTATCTA	720
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Db	781	CTGTTGGGGATATATGACACATCACTACG3GTTTGGAG3TCTGGGGGCAAAGGACACAGGTC	840
OY	841	ACCGTCTCTTCAGAGATCCGAAACAAAACATGATCAGCGAAGAAAGATGTGAACCATCAACAT	900
Db	841	ACCGTCTCTTCAGAGATCCGAAACAAAACATGATCAGCGAAGAAAGATGTGAACCATCAACAT	900
OY	901	CACCATTAAGTGAAGCTT 918	
Db	901	CACCATTAAGTGAAGCTT 918	

```

:
: TELEPHONE: (650) 913-5600
:
: TELEFAX: (650) 494-0792
:
: TELEXT: 706141
:
: INFORMATION FOR SEQ ID NO: 13:
:
: SEQUENCE CHARACTERISTICS:
:
: LENGTH: 918 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: FEATURE:
:
: NAME/KEY: CDS
:
: LOCATION: join(1..906, 913..918)
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 13:
:
US-09-782-397B-13

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Db 781 CTGTTGGGTGACATATACCACTAAGGTTGGAGCTCTGGGGCAAGGACCACGCTC 840
 Qy 841 ACCGTCCTCCTCAGATCCGAAACAAAATGATCAGGCAAGAGATCTGAACATCACCAT 900
 Db 841 ACCGTCCTCCTCAGATCCGAAACAAAATGATCAGGCAAGAGATCTGAACATCACCAT 900
 Qy 901 CACCATTTAGTGAAGCTT 918
 Db 901 CACCATTTAGTGAAGCTT 918

RESULT 7

US-09-782-397C-13
 / Sequence 13, Application US/09782397C
 / GENERAL INFORMATION:
 / APPLICANT: Valentia Biotech Inc.
 / APPLICANT: Dan, Michael D.
 / APPLICANT: Maif, Pradip K.
 / APPLICANT: Kaplan, Howard A.
 / TITLE OF INVENTION: Antigen Binding Fragments that Specifically Detect Cancer Cells.
 / FILE REFERENCE: 830001-2001.2
 / CURRENT APPLICATION NUMBER: US/09/782,397C
 / PRIOR FILING DATE: 2001-02-13
 / PRIOR APPLICATION NUMBER: 08/662,124
 / PRIOR FILING DATE: 1997-05-22
 / PRIOR APPLICATION NUMBER: 08/657,449
 / PRIOR FILING DATE: 1996-05-22
 / NUMBER OF SEQ ID NOS: 29
 / SOFTWARE: Patent version 3.1
 / SEQ ID NO 13
 / LENGTH: 918
 / TYPE: DNA
 / ORGANISM: homo sapien
 / FEATURE:
 / NAME/KEY: CDS
 / LOCATION: (1)..(906)
 / OTHER INFORMATION:
 / NAME/KEY: CDS
 / LOCATION: (913)..(918)
 / OTHER INFORMATION:
 / US-09-782-397C-13

Query Match 100.0%; Score 918; DB 33; Length 918;
 Best Local Similarity 100.0%; Pred. No. 2,5e-225;
 Matches 918; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCATGAAAAAACCCCTATCGGATCGAGTTGCACTGCTGCTTTCGCTACCGTT 60
 Db 1 GAATTCATGAAAAAACCCCTATCGGATCGAGTTGCACTGCTGCTTTCGCTACCGTT 60
 Qy 61 GGGGAGGCGGATATGTTGTGAGCGAGTCTCCAGGACCCCTGTTTGTCTCAAGGGAA 120
 Db 61 GGGGAGGCGGATATGTTGTGAGCGAGTCTCCAGGACCCCTGTTTGTCTCAAGGGAA 120
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 Db 121 AGAGCCACCTCTCTCTGCAAGGCGAGTCAAGTGTAGTAGCAGTACTTACCTGTAC 180
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 Qy 181 CAGCAAAAAGCTGGCCAGGCTCCAGGCTCTCATCTATGTGATCCACAGGGCACT 240
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 Qy 241 GGCATGCCGAGAGGTTGAGTGGGAGTGGGTCGGGAGACAGTTCATCTTCACATCACT 300
 Db 241 GGCATGCCGAGAGGTTGAGTGGGAGTGGGTCGGGAGACAGTTCATCTTCACATCACT 300
 Qy 301 AGACTGAGACCTGAAGATTTCAGTGTATTACTGTCAAGAGTATGATCACTCAG 360
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 Qy 361 AACCTCAGATCACTTTGGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 420
 Db 361 AACCTCAGATCACTTTGGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 420

Db 361 AACCTCAGATCACTTTGGCGAGGAGCAAGGTGAGATCAAGAACTGTGCTGCA 420
 Qy 421 CCATCTGTCTGGGCGTGGCGTTCCGAGGTGGATTCAGGTGAGTGGCTCCGAG 480
 Db 421 CCATCTGTCTGGGCGTGGCGTTCCGAGGTGGATTCAGGTGAGTGGCTCCGAG 480
 Qy 481 GTGAGCTGTGAGTCTGGGAGGCGGTGTCTCAGCCTGGAGGCTCCAGACTTCC 540
 Db 481 GTGAGCTGTGAGTCTGGGAGGCGGTGTCTCAGCCTGGAGGCTCCAGACTTCC 540
 Qy 541 TGTGAGCTCTTGATTTCCCTTCAAGAGCTTGTCTATGCACTGGTCCGAGCTCTA 600
 Db 541 TGTGAGCTCTTGATTTCCCTTCAAGAGCTTGTCTATGCACTGGTCCGAGCTCTA 600
 Qy 601 GGCAGAGGCGTGGAGTGGTGGCACTTATATCATATGATGAGCACTAAATACACGA 660
 Db 601 GGCAGAGGCGTGGAGTGGTGGCACTTATATCATATGATGAGCACTAAATACACGA 660
 Qy 661 GACTCGTGAAAGGCGCATTCACATCTCCAGAGACACTTCCAGAACACGCTGTATCTA 720
 Db 661 GACTCGTGAAAGGCGCATTCACATCTCCAGAGACACTTCCAGAACACGCTGTATCTA 720
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 Db 721 AAAATGAACGCTTGAAGACTGAGACACGCTGTCTATTACTGTGCGAGATCAGAC 780
 Qy 781 CTGTTGGGTGATATGACCACTACCTAGCTTGAAGTGGGCAAGGACCAAGCTC 840
 Db 781 CTGTTGGGTGATATGACCACTACCTAGCTTGAAGTGGGCAAGGACCAAGCTC 840
 Qy 841 ACCGTCCTCCTCAGATCCGAAACAAAATGATCAGGAAAGATCTGAACATCACCAT 900
 Db 841 ACCGTCCTCCTCAGATCCGAAACAAAATGATCAGGAAAGATCTGAACATCACCAT 900
 Qy 901 CACCATTTAGTGAAGCTT 918
 Db 901 CACCATTTAGTGAAGCTT 918

RESULT 8

US-08-657-449-15/C
 / Sequence 15, Application US/08657449
 / GENERAL INFORMATION:
 / APPLICANT: Dan, Michael D.
 / APPLICANT: Maif, Pradip K.
 / APPLICANT: Kaplan, Howard A.
 / TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND NUMBER OF SEQUENCES: 18
 / CORRESPONDENCE ADDRESS:
 / ADDRESSER: Morrison & Foerster
 / STREET: 755 Page Mill Road
 / CITY: Palo Alto
 / STATE: CA
 / COUNTRY: USA
 / ZIP: 94304-1018
 / COMPUTER READABLE FORM:
 / MEDIUM TYPE: Floppy disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: Patent in Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/657,449
 / FILING DATE:
 / CLASSIFICATION: 424
 / ATTORNEY/AGENT INFORMATION:
 / NAME: lehnhardt, Susan K.
 / REGISTRATION NUMBER: 33,943
 / REFERENCE/DOCKET NUMBER: 31608-20001.00
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792
 TELEEX: 706141
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 918 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-657-449-15

Query Match 99.8%; Score 916.4; DB 11; Length 918;
 Best Local Similarity 99.9%; Pred. No. 6.5e-225;
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GAATTCATGAAAAAACCCTATCGCGATGCGAGTTGCACTGCTGGTTTGGTACCGTT 60
DB 918 GAATTCATGAAAAAACCCTATCGCGATGCGAGTTGCACTGCTGGTTTGGTACCGTT 859
QY 61 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCTCTGTTTGTCTCCAGGGGAA 120
DB 858 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCTCTGTTTGTCTCCAGGGGAA 799
QY 121 AGAGCCACCTCTCTCGAGGGGCGAGTCAAGTGTAGTAGAGCTACTTACCTGGTAC 180
DB 798 AGAGCCACCTCTCTCTCGAGGGGCGAGTCAAGTGTAGTAGAGCTACTTACCTGGTAC 739
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGATCCACGAGGCCACT 240
DB 738 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGATCCACGAGGCCACT 679
QY 241 GGCATGCGCAGACAGGTTCAAGTGGAGTGGTCCGGGACAGCTTCACTTCCACCATAGT 300
DB 678 GGCATGCGCAGACAGGTTCAAGTGGAGTGGTCCGGGACAGCTTCACTTCCACCATAGT 619
QY 301 AGACTGAGGCTGTAAGATTTTGCAGTGTATCTGTACAGAGTATGTTAGTCACTACCTAG 360
DB 618 AGACTGAGGCTGTAAGATTTTGCAGTGTATCTGTACAGAGTATGTTAGTCACTACCTAG 559
QY 361 ACACCTGAGTCACTTTTCGCGGAGGAGCAAGGTGAGATCAAAACGAACTGTGGTGA 420
DB 558 ACACCTGAGTCACTTTTCGCGGAGGAGCAAGGTGAGATCAAAACGAACTGTGGTGA 499
QY 421 CCATCTGCTCTGCGCGGTGGTTCGCGAGTGTGTGAATGAGTGGAGTGGTCCAG 480
DB 498 CCATCTGCTCTGCGCGGTGGTTCGCGAGTGTGTGAATGAGTGGAGTGGTCCAG 439
QY 481 GTGACGCTGTGAGTCTGCGGGGAGGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCC 540
DB 438 GTGACGCTGTGAGTCTGCGGGGAGGCGTGTCCAGCTGGAGAGTCCCTGAGACTCTCC 379
QY 541 TGTGACGCTGTGAGTCTCCCTTCAGAAAGCTTTGCTATGCACTGGGTCCGCAAGCTCTA 600
DB 378 TGTGACGCTGTGAGTCTCCCTTCAGAAAGCTTTGCTATGCACTGGGTCCGCAAGCTCTA 319
QY 601 GCGAAGGGGCTGAGTGGTGGAGTATATCATATATGTAAGACACTAAATACATGAGCA 660
DB 318 GCGAAGGGGCTGAGTGGTGGAGTATATCATATATGTAAGACACTAAATACATGAGCA 259
QY 661 GACTCCGTAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACCGGTGTATTA 720
DB 258 GACTCCGTAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAAGAACCGGTGTATTA 199
QY 721 AAAATGAAACAGCTGAGAACTGAGAGACACGCGTGTCTATTAATCTGTGCGAGAGATCAG 780
DB 198 AAAATGAAACAGCTGAGAACTGAGAGACACGCGTGTCTATTAATCTGTGCGAGAGATCAG 139
QY 781 CTGTTGGGTGACTATAGACCACTACTACGTTTGGACGCTGGGGGAAAGGAGACACGCTC 840
DB 138 CTGTTGGGTGACTATAGACCACTACTACGTTTGGACGCTGGGGGAAAGGAGACACGCTC 79
QY 841 ACCGCTCTCTAGATCCGAAACAAACCTGATCAGCGAAGAGATCTGAACCATCATCAT 900
DB 78 ACCGCTCTCTAGATCCGAAACAAACCTGATCAGCGAAGAGATCTGAACCATCATCAT 19
  
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QY 901 CACCATTAAGTGAAGCTT 918
 DB 18 CACCATTAAGTGAAGCTT.1

RESULT 9

US-09-697-561-15/C
 Sequence 15, Application US/09697561

GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 Malt, Pradip K.
 Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:

ADDRESSER: Morrison & Foerster LLP

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/697,561

FILING DATE: 26-Oct-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/862,124

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:

TELEPHONE: (650) 813-5600

TELEFAX: (650) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 918 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:

US-09-697-561-15

Query Match 99.8%; Score 916.4; DB 30; Length 918;

Best Local Similarity 99.9%; Pred. No. 6.5e-225;

Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 GAATTCATGAAAAAACCCTATCGCGATGCGAGTTGCACTGCTGGTTTGGTACCGTT 60
DB 918 GAATTCATGAAAAAACCCTATCGCGATGCGAGTTGCACTGCTGGTTTGGTACCGTT 859
QY 61 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCTCTGTTTGTCTCCAGGGGAA 120
DB 858 GCGCAGGCCGATATGTTGTTGACGCACTCTCCAGGACCTCTGTTTGTCTCCAGGGGAA 799
QY 121 AGAGCCACCTCTCTCGAGGGGCGAGTCAAGTGTAGTAGAGCTACTTACCTGGTAC 180
DB 798 AGAGCCACCTCTCTCTCGAGGGGCGAGTCAAGTGTAGTAGAGCTACTTACCTGGTAC 739
QY 181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGATCCACGAGGCCACT 240
DB 738 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTTGATCCACGAGGCCACT 679
  
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QY 241 GGCATGCCAGACAGGTTCACTGACAGTGGGTCCTCCGGACACAGACTTCACTTCAACCATCACT 300
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DB 678 GGCATGCCAGACAGGTTCACTGACAGTGGGTCCTCCGGACACAGACTTCACTTCAACCATCACT 619
QY 301 AGACTGGAGCCTGGAAGATTTTGGAGTGTATTACTGTACAGAGATAGTGTAGCTTCACTTCACT 360
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DB 618 AGACTGGAGCCTGGAAGATTTTGGAGTGTATTACTGTACAGAGATAGTGTAGCTTCACTTCACT 559
QY 361 ACACCTCAGATCACTTTCGGCGGAGGAGCCAAAGTGAATCAAAAGAACTGTGTGCA 420
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DB 558 ACACCTCAGATCACTTTCGGCGGAGGAGCCAAAGTGAATCAAAAGAACTGTGTGCA 499
QY 421 CCATCTGTCTGTGCGGTGGCGGTTCGGAGGTGTGATCAAGTGAAGTGTGCTCCAG 480
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DB 498 CCATCTGTCTGTGCGGTGGCGGTTCGGAGGTGTGATCAAGTGAAGTGTGCTCCAG 439
QY 481 GTGCAAGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 540
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DB 438 GTGCAAGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 379
QY 541 TGTGAGCCTCTGAGATTTCCCTTCAAGACCTTGTATGATCACTGAGTGTGCTCCAG 600
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DB 378 TGTGAGCCTCTGAGATTTCCCTTCAAGACCTTGTATGATCACTGAGTGTGCTCCAG 319
QY 601 GGCAGAGGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 660
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DB 318 GGCAGAGGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 259
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DB 258 GACTCCGTGAAGAGGCGGATTTCACTCTCAAGAGACCTTCCAAAGACCGGTGTGCT 199
QY 721 AAAATGAACAGCCTGGAAGCTGAGGACAGGCTGTATTACTGTGCGAGATCGAGC 780
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DB 198 AAAATGAACAGCCTGGAAGCTGAGGACAGGCTGTATTACTGTGCGAGATCGAGC 139
QY 781 CTGTTGGGTGATGACCACTACTACGCTTGTGAGCGTCTGGGCGCAAGGAGCAAGCT 840
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DB 138 CTGTTGGGTGATGACCACTACTACGCTTGTGAGCGTCTGGGCGCAAGGAGCAAGCT 79
QY 841 ACCGCTCTCTCAGATCCGAAACAAAACTGATCAGGAGAAAGATTTGAACATCACT 900
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DB 78 ACCGCTCTCTCAGATCCGAAACAAAACTGATCAGGAGAAAGATTTGAACATCACT 19
QY 901 CACCATTAGTGAAGCTT 918
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DB 18 CACCATTAGTGAAGCTT 1
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RESULT 10
US-09-697-561A-15/c
; Sequence 15, Application US/09697561A
; GENERAL INFORMATION:
; APPLICANT: Viventia Biotech Inc.
; APPLICANT: Dan, Michael D
; APPLICANT: Maeli, Pradip K
; APPLICANT: Kaplan, Howard A.
; TITLE OF INVENTION: Antigen Binding Fragments that Specifically Detect Cancer Cells,
; TITLE OF INVENTION: Nucleotides Encoding the Fragments...
; FILE REFERENCE: 830001-2001.1
; CURRENT FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: 08/862,124
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-697-561A-15
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Query Match 99.8%; Score 916.4; DB 30; Length 918;
Best Local Similarity 99.8%; Pred. No. 6,5e-225;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCAGAAAAAACCGCTATCCGAGATCCGAGTGTGCACTGCGTGTTCCTACCGTT 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 918 GAATTCAGAAAAAACCGCTATCCGAGATCCGAGTGTGCACTGCGTGTTCCTACCGTT 859
QY 61 GCGCAGGCGGATATTGTGTGACGCAAGTCTCAGAGCAACCTCTTGTGTCTCAAGGAGAA 120
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DB 858 GCGCAGGCGGATATTGTGTGACGCAAGTCTCAGAGCAACCTCTTGTGTCTCAAGGAGAA 799
QY 121 AGAGCCACCCTCTCTCTGCAAGGCGCACTCAGAGTGTGATGAGCACTTAACTGCTGAT 180
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DB 798 AGAGCCACCCTCTCTCTGCAAGGCGCACTCAGAGTGTGATGAGCACTTAACTGCTGAT 739
QY 181 CAGCAAAAACTTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGCGCACT 240
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DB 738 CAGCAAAAACTTGGCCAGGCTCCAGGCTCTCATCTATGTGTGATCCACAGGCGCACT 679
QY 241 GGCATGCCAGACAGGTTCACTGACAGTGGGTCCTCCGGACACAGACTTCACTTCAACCATCACT 300
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DB 678 GGCATGCCAGACAGGTTCACTGACAGTGGGTCCTCCGGACACAGACTTCACTTCAACCATCACT 619
QY 301 AGACTGGAGCCTGGAAGATTTTGGAGTGTATTACTGTACAGAGATAGTGTAGCTTCACTTCACT 360
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DB 618 AGACTGGAGCCTGGAAGATTTTGGAGTGTATTACTGTACAGAGATAGTGTAGCTTCACTTCACT 559
QY 361 ACACCTCAGATCACTTTCGGCGGAGGAGCCAAAGTGAATCAAAAGAACTGTGTGCA 420
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DB 558 ACACCTCAGATCACTTTCGGCGGAGGAGCCAAAGTGAATCAAAAGAACTGTGTGCA 499
QY 421 CCATCTGTCTGTGCGGTGGCGGTTCGGAGGTGTGATCAAGTGTGAGTGTGCTCCAG 480
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DB 498 CCATCTGTCTGTGCGGTGGCGGTTCGGAGGTGTGATCAAGTGTGAGTGTGCTCCAG 439
QY 481 GTGCAAGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 540
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 438 GTGCAAGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 379
QY 541 TGTGAGCCTCTGAGATTTCCCTTCAAGACCTTGTATGATCACTGAGTGTGCTCCAG 600
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DB 378 TGTGAGCCTCTGAGATTTCCCTTCAAGACCTTGTATGATCACTGAGTGTGCTCCAG 319
QY 601 GGCAGAGGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 660
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DB 318 GGCAGAGGCTGTGAGTGTGCGGAGGAGCGGTGTGATCAAGTGTGAGTGTGCTCCAG 259
QY 661 GACTCCGTGAAGAGGCGGATTTCACTCTCAAGAGACCTTCCAAAGACCGGTGTGCT 720
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DB 258 GACTCCGTGAAGAGGCGGATTTCACTCTCAAGAGACCTTCCAAAGACCGGTGTGCT 199
QY 721 AAAATGAACAGCCTGGAAGCTGAGGACAGGCTGTATTACTGTGCGAGATCGAGC 780
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 198 AAAATGAACAGCCTGGAAGCTGAGGACAGGCTGTATTACTGTGCGAGATCGAGC 139
QY 781 CTGTTGGGTGATGACCACTACTACGCTTGTGAGCGTCTGGGCGCAAGGAGCAAGCT 840
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 138 CTGTTGGGTGATGACCACTACTACGCTTGTGAGCGTCTGGGCGCAAGGAGCAAGCT 79
QY 841 ACCGCTCTCTCAGATCCGAAACAAAACTGATCAGGAGAAAGATTTGAACATCACT 900
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DB 78 ACCGCTCTCTCAGATCCGAAACAAAACTGATCAGGAGAAAGATTTGAACATCACT 19
QY 901 CACCATTAGTGAAGCTT 918
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DB 18 CACCATTAGTGAAGCTT 1
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 11
US-09-782-397-15/c
; Sequence 15, Application US/09782397
; GENERAL INFORMATION:
```


APPLICANT: Dan, Michael D.
Maltz, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/862,124
FILING DATE: 1997-05-22
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 813-5600
TELEFAX: (650) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-782-397-15
Query Match 99.8%; Score 916.4; DB 33; Length 918;
Best Local Similarity 99.9%; Pred. No. 6.5e-225; Indels 0; Gaps 0;
Matches 917; Conservative 0; Mismatches 1;
1 GAATTCATGAAAAAACCCTATCGCATCGCATGTCAGTGGCTGTTGGCTACCGTT 60
2 918 GAATTCATGAAAAAACCCTATCGCATCGCATGTCAGTGGCTGTTGGCTACCGTT 859
3 61 GCGCAGGCGCATATGTTGTTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGAA 120
4 858 GCGCAGGCGCATATGTTGTTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGAA 799
5 121 AAGGCCACCTCTCTCTGCGAGGCGCATGAGTGTATGAGAGAGTACTTGGCTGATAC 180
6 798 AAGGCCACCTCTCTCTGCGAGGCGCATGAGTGTATGAGAGAGTACTTGGCTGATAC 739
7 181 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCACGAGGCACT 240
8 738 CAGCAGAACTGGCCAGGCTCCAGGCTCTCATCTATGATGATCCACGAGGCACT 679
9 241 GGCATGCCAGACAGGTTCACTGAGTGGCTGCGGAGCAGACTTCACTTCCACATCACT 300
10 678 GGCATGCCAGACAGGTTCACTGAGTGGCTGCGGAGCAGACTTCACTTCCACATCACT 619
11 301 AAGCTGAGCTGTAAGATTTGAGTGTATTAATCTGACAGATGATGATGATGATGATGAT 360
12 618 AAGCTGAGCTGTAAGATTTGAGTGTATTAATCTGACAGATGATGATGATGATGATGATGAT 559
13 361 ACACCTCAGATCACTTTCGCGGAGGAGCCAAAGTGGAGATCAAAAGAACTGTGCTGCA 420

558 ACACCTCAGATCACTTTCGCGGAGGAGCCAAAGTGGAGATCAAAAGAACTGTGCTGCA 499
421 CCATCTGCTCTGCGCGGTGGCGGTTCCGGAGGTGTGATGATGATGATGATGATGATGATGAT 480
498 CCATCTGCTCTGCGCGGTGGCGGTTCCGGAGGTGTGATGATGATGATGATGATGATGATGAT 439
481 GTGAGCTGTGTGAGTCTGCGGAGGAGCGTGTGATGATGATGATGATGATGATGATGATGAT 540
438 GTGAGCTGTGTGAGTCTGCGGAGGAGCGTGTGATGATGATGATGATGATGATGATGATGAT 379
541 TGTGAGCTGTGTGAGTCTGCGGAGGAGCGTGTGATGATGATGATGATGATGATGATGATGAT 600
378 TGTGAGCTGTGTGAGTCTGCGGAGGAGCGTGTGATGATGATGATGATGATGATGATGATGAT 319
601 GGCAGAGGCGTGTGAGTCTGCGGAGGAGCGTGTGATGATGATGATGATGATGATGATGATGAT 660
318 GGCAGAGGCGTGTGAGTCTGCGGAGGAGCGTGTGATGATGATGATGATGATGATGATGATGAT 259
661 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAGACAGGCTGATCTA 720
258 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAGACAGGCTGATCTA 199
721 AAATGAACAGCTGAGAACTGAGAGCAAGCTGCTATTAATCTGCGAGATGAGAGC 780
198 AAATGAACAGCTGAGAACTGAGAGCAAGCTGCTATTAATCTGCGAGATGAGAGC 139
781 CTTGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 840
138 CTTGTTGGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 79
841 ACCGTCCTCTCAGATTCGAGCAAACTGATGAGAGAAAGATGATGATGATGATGATGATGAT 900
78 ACCGTCCTCTCAGATTCGAGCAAACTGATGAGAGAAAGATGATGATGATGATGATGATGAT 19
901 CACCATTAAGTGAAGCTT 918
18 CACCATTAAGTGAAGCTT 1
RESULT 12
US-09-782-397A-15/c
Sequence 15, Application US/09782397A
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Maltz, Pradip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster LLP
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/782,397A
FILING DATE: 13-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/862,124
FILING DATE: 22-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Lehnardt, Susan K.

REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 31608-20001.20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 918 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-09-782-397A-15

Query Match 99.8%; Score 916.4; DB 33; Length 918;
 Best Local Similarity 99.9%; Pred. No. 6.5e-225;
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAATTCATGAAAAAACCCTATCGCGATCGAGTTCAGCTGCTGCTTCCGTACCGTT 60
 918 GAATTCATGAAAAAACCCTATCGCGATCGAGTTCAGCTGCTGCTTCCGTACCGTT 859

61 GGGCAGGCCGATATTGTGTGAGCGAGTCTCCAGGCACTGCTTGTCTCCAGGGGAA 120
 858 GGGCAGGCCGATATTGTGTGAGCGAGTCTCCAGGCACTGCTTGTCTCCAGGGGAA 799

121 AGAGCCACCCTCTCTGCAAGGGGAGTCAGAGTGTAGTAGCACTTAAAGCTGTATC 180
 798 AGAGCCACCCTCTCTGCAAGGGGAGTCAGAGTGTAGTAGCACTTAAAGCTGTATC 739

181 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCAACAGGGCCACT 240
 738 CAGCAGAAACCTGCGCAGGCTCCAGGCTCTCATCTATGTGATCAACAGGGCCACT 679

241 GGCATGCCAGACAGGTTCACTGAGTGGTCCGGGACAGACTTCACTCTACCATGAGT 300
 678 GGCATGCCAGACAGGTTCACTGAGTGGTCCGGGACAGACTTCACTCTACCATGAGT 619

301 AGACTGAGACCTGGAAGATTTTGAGTGTATTACTGTCAAGATGATGTAGTCACTCAG 360
 618 AGACTGAGACCTGGAAGATTTTGAGTGTATTACTGTCAAGATGATGTAGTCACTCAG 559

361 ACACCTCAGATCACTTTCGCGGAGGAGCAAGGTGAGTCAAGCACTGTGCTGCA 420
 558 ACACCTCAGATCACTTTCGCGGAGGAGCAAGGTGAGTCAAGCACTGTGCTGCA 499

421 CCATCTGTCTTGGCGGTGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 480
 498 CCATCTGTCTTGGCGGTGCGGTTCCGAGGTGTGATCAGGTGAGGTGCTCCAG 439

481 GTGCACTGTGAGTCTGCGGAGGAGGCTGTCCAGCTGGAGGCTCCAGACTCTCC 540
 438 GTGCACTGTGAGTCTGCGGAGGAGGCTGTCCAGCTGGAGGCTCCAGACTCTCC 379

541 TGTGCACTGTGAGTCTCCCTTCAGAACTTGTCTATCACTGAGTCCGCGAGCTCTA 600
 378 TGTGCACTGTGAGTCTCCCTTCAGAACTTGTCTATCACTGAGTCCGCGAGCTCTA 319

601 GGCAGAGGCTGAGTGGTGGGAGGATTAATCATATGATGAGAGCACTAAATCTACGCA 660
 318 GGCAGAGGCTGAGTGGTGGGAGGATTAATCATATGATGAGAGCACTAAATCTACGCA 259

661 GACTCCGTAAGGGCCGATTCACCATCTCCAGAGACCTTCCAGAAACCGGTATCTTA 720
 258 GACTCCGTAAGGGCCGATTCACCATCTCCAGAGACCTTCCAGAAACCGGTATCTTA 199

721 AAAATGAAGCCTGAGAACTGAGACAGGCTGTCTATTAATCTGTCGAGAGATCAGAGC 780
 198 AAAATGAAGCCTGAGAACTGAGACAGGCTGTCTATTAATCTGTCGAGAGATCAGAGC 139

781 CTGTTGGGTGACTATGACCACTTACGCTTTGAGAGCTGTGAGGCAAGGAGCAACGCTC 840

Db 138 CTGTTGGGTGACTATGACCACTACTAGGTTTGGAGCTTGGGGCAAGGAGCAACGCTC 79
 841 ACCGTTCTCTCAGAGATCCGACAAAAAATGATCAGGAGAGATGTGACCATCAGCAT 900
 Db 78 ACCGTTCTCTCAGAGATCCGACAAAAAATGATCAGGAGAGATGTGACCATCAGCAT 19

Qy 901 CACCATTAAGTGAAGCTT 918
 Db 18 CACCATTAAGTGAAGCTT 1

RESULT 13

US-09-782-397B-15/C
 ; Sequence 15, Application US/09782397B
 ; GENERAL INFORMATION:
 ; APPLICANT: Dan, Michael D.
 ; Maiti, Pradip K.
 ; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS H1, THAT
 ; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES
 ; ENCODING THE
 ; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND

NUMBER OF SEQUENCES: 28
 CORRESPONDENCE ADDRESS:
 ADDRESSER: Morrison & Foerster LLP
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/782,397B
 FILING DATE: 13-Feb-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/862,124
 FILING DATE: 1997-05-22

ATTORNEY/AGENT INFORMATION:
 NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 31608-20001.20

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (650) 813-5600
 TELEFAX: (650) 494-0792
 TELEX: 706141

INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 918 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 US-09-782-397B-15

Query Match 99.8%; Score 916.4; DB 33; Length 918;
 Best Local Similarity 99.9%; Pred. No. 6.5e-225;
 Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1 GAATTCATGAAAAAACCCTATCGCGATCGAGTTCAGCTGCTGCTTCCGTACCGTT 60
 918 GAATTCATGAAAAAACCCTATCGCGATCGAGTTCAGCTGCTGCTTCCGTACCGTT 859

61 GGCAGGCCGATATTGTGTGAGCGAGTCTCCAGGCACTGCTTGTCTCCAGGGGAA 120
 858 GGCAGGCCGATATTGTGTGAGCGAGTCTCCAGGCACTGCTTGTCTCCAGGGGAA 799

121 AGAGCCACCCTCTCTGCAAGGGGAGTCAGAGTGTAGTAGCACTTAAAGCTGTATC 180

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Db      798 AGAGGACACCTCTCTCTGACAGGGCCAGTACAGTATTAGTACAGTACTTACGCTGGTAC 739
Qy      181 CAGCAGAAACCTTGCCAGGCTCCCAAGGCTCTCTATCTATGGTGATCACACAGGCTACT 240
Db      738 CACGACAAACCTTGCCAGGCTCCCAAGGCTCTCTATCTATGGTGATCACACAGGCTACT 679
Qy      241 GGCATGCGACAGGTTGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 300
Db      678 GGCATGCGACAGGTTGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 619
Qy      301 AGACTGAGGCTTGAAGATTTTTCAGTGTATTAATCTGTACAGATGATGATGATGATGATGATGAT 360
Db      618 AGACTGAGGCTTGAAGATTTTTCAGTGTATTAATCTGTACAGATGATGATGATGATGATGATGAT 559
Qy      361 ACACCTTCAATCACTTTTCGCGAGAGGACCAAGTGAATCAAAACCAACTGTGGCTGCA 420
Db      558 ACACCTTCAATCACTTTTCGCGAGAGGACCAAGTGAATCAAAACCAACTGTGGCTGCA 499
Qy      421 CCATCTGCTCTGCGGAGGAGTTCGGAAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 480
Db      498 CCATCTGCTCTGCGGAGGAGTTCGGAAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 439
Qy      481 GTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 540
Db      438 GTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 379
Qy      541 TGTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 600
Db      378 TGTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 319
Qy      601 GGCAAGGGGCTGAGTGGGAGGAGTGGTGGATCATATATGATGATGATGATGATGATGATGATGAT 660
Db      318 GGCAAGGGGCTGAGTGGGAGGAGTGGTGGATCATATATGATGATGATGATGATGATGATGATGAT 259
Qy      661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCACTTCAAGAAACGCGTGTATCTA 720
Db      258 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCACTTCAAGAAACGCGTGTATCTA 199
Qy      721 AAAATGAACAGCTGAGAACTGAGAGACACGCGTGTATCTA 780
Db      198 AAAATGAACAGCTGAGAACTGAGAGACACGCGTGTATCTA 139
Qy      781 CTGTTGGGTGACTATGACCACTACAGTGGTGGAGTGGGCAAAAGGAGCCAGCGTCT 840
Db      138 CTGTTGGGTGACTATGACCACTACAGTGGTGGAGTGGGCAAAAGGAGCCAGCGTCT 79
Qy      841 ACCGCTCTCTCAGGATCCGAAACAAAACCTGATCAGCGAAGATCTGAACCATCACCAT 900
Db      78 ACCGCTCTCTCAGGATCCGAAACAAAACCTGATCAGCGAAGATCTGAACCATCACCAT 19
Qy      901 CACCATTAAGTGAAGCTT 918
Db      18 CACCATTAAGTGAAGCTT 1

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; SOFTWARE: Patentin version 3.1
; SEQ ID NO 15
; LENGTH: 918
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-782-397C-15

Query Match      99.8%; Score 916.4; DB 33; Length 918;
Best Local Similarity 99.9%; Pred. No. 6.5e-225;
Matches 917; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db      918 GAATTCATGAAAAAAACCGCTATCCGATGCGAGTTGCACTGGCTGGTTCCGTAACCTT 859
Qy      61 GCGCAGGCGGATTTGTTGTTGAGCGAGTCCAGGACCTGCTTGTCTCCAGGGGAA 120
Db      858 GCGCAGGCGGATTTGTTGTTGAGCGAGTCCAGGACCTGCTTGTCTCCAGGGGAA 799
Qy      121 AGAGCACCTCTCTGACAGGCGCAGTCAAGTGTATGAGCACTAATTAAGCTGGTAC 180
Db      798 AGAGGACCTCTCTCTGACAGGCGCAGTCAAGTGTATGAGCACTAATTAAGCTGGTAC 739
Qy      181 CACGACAAACCTTGCCAGGCTCCCAAGGCTCTCTATCTATGGTGATCACACAGGCTACT 240
Db      738 CACGACAAACCTTGCCAGGCTCCCAAGGCTCTCTATCTATGGTGATCACACAGGCTACT 679
Qy      241 GGCATGCGACAGGTTGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 300
Db      678 GGCATGCGACAGGTTGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGTGGGAGT 619
Qy      301 AGACTGAGGCTTGAAGATTTTTCAGTGTATTAATCTGTACAGATGATGATGATGATGATGATGAT 360
Db      618 AGACTGAGGCTTGAAGATTTTTCAGTGTATTAATCTGTACAGATGATGATGATGATGATGATGAT 559
Qy      361 ACACCTTCAATCACTTTTCGCGAGAGGACCAAGTGAATCAAAACCAACTGTGGCTGCA 420
Db      558 ACACCTTCAATCACTTTTCGCGAGAGGACCAAGTGAATCAAAACCAACTGTGGCTGCA 499
Qy      421 CCATCTGCTCTGCGGAGGAGTTCGGAAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 480
Db      498 CCATCTGCTCTGCGGAGGAGTTCGGAAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 439
Qy      481 GTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 540
Db      438 GTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 379
Qy      541 TGTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 600
Db      378 TGTGACGCTGTGAGTCTGCGGAGGAGTGGTGGATCAGGTGAGGAGTGGCTCCAG 319
Qy      601 GGCAAGGGGCTGAGTGGGAGGAGTGGTGGATCATATATGATGATGATGATGATGATGATGATGAT 660
Db      318 GGCAAGGGGCTGAGTGGGAGGAGTGGTGGATCATATATGATGATGATGATGATGATGATGATGAT 259
Qy      661 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCACTTCAAGAAACGCGTGTATCTA 720
Db      258 GACTCCGTGAAGGGCCGATTCACCATCTCCAGAGCACTTCAAGAAACGCGTGTATCTA 199
Qy      721 AAAATGAACAGCTGAGAACTGAGAGACACGCGTGTATCTA 780
Db      198 AAAATGAACAGCTGAGAACTGAGAGACACGCGTGTATCTA 139
Qy      781 CTGTTGGGTGACTATGACCACTACAGTGGTGGAGTGGGCAAAAGGAGCCAGCGTCT 840
Db      138 CTGTTGGGTGACTATGACCACTACAGTGGTGGAGTGGGCAAAAGGAGCCAGCGTCT 79
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Qy      901 CACCATTAAGTGAAGCTT 918

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Db 18 CACCATTAAGTGAAGCTT 1

RESULT 15
US-08-657-449-16
Sequence 16, Application US/08657449
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
APPLICANT: Malt, Pradip K.
APPLICANT: Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
SPECIFICALLY DETECT CANCER CELLS
TITLE OF INVENTION: FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
TREATMENT OF CANCERS
TITLE OF INVENTION: DETECTION OF CANCERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/657,449
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Leinhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ. ID NO.: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: join(1..855, 862..867)
US-08-657-449-16

Query Match 87.1%; Score 799.6; DB 11; Length 867;
Best Local Similarity 94.0%; Pred. No. 7.4e-195;
Matches 863; Conservative 0; Mismatches 4; Indels 51; Gaps 1;

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QY 121 AGAGCACCCTCTCTGCGAGGCGAGTCAAGAGTATTAGCAGCTACTAGCTGATG 180
DB 121 AGAGCACCCTCTCTGCGAGGCGAGTCAAGAGTATTAGCAGCTACTAGCTGATG 180

QY 181 CAGCAGAAAACCTGCGCAGGCTCCAGAGCTCTCATCTATGATGATCAACAGAGCCACT 240
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QY 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGGACAGACTTCACTGACCATCACT 300
DB 241 GGCATGCCAGACAGGTTCACTGAGTGGGTCCGGGACAGACTTCACTGACCATCACT 300

QY 301 AGACTGAGCCCTGAAAGATTTTGCAGTGTATTAATCTGTACAGAGTATGATGATCACTCAG 360
DB 301 AGACTGAGCCCTGAAAGATTTTGCAGTGTATTAATCTGTACAGAGTATGATGATCACTCAG 360

QY 361 ACACCTCAATCACTTTGCGCGGAGGAGCAGCAGAGTGAATCAAGAACTGTGGCTGCA 420
DB 361 ACACCTCAATCACTTTGCGCGGAGGAGCAGCAGAGTGAATCAAGAACTGTGGCTGCA 420

QY 421 CCATCTGTCTGCGCGGAGGAGTTCGAGAGTGGATCAAGTGGAGTGGCTCCAG 480
DB 421 TC-----CGAGCAG 429

QY 481 GTGCACTGTGAGAGTCTGCGGAGGAGCTGTGCTCACTGAGAGTCCCTGAGACTCTCC 540
DB 430 GTGCACTGTGAGAGTCTGCGGAGGAGCTGTGCTCACTGAGAGTCCCTGAGACTCTCC 489

QY 541 TGTGCAAGCTCTGAGATTCCTCTTCAAGAGCTTTGTATGCACTGGGTCCGCGAGCTCTA 600
DB 490 TGTGCAAGCTCTGAGATTCCTCTTCAAGAGCTTTGTATGCACTGGGTCCGCGAGCTCTA 549

QY 601 GGCAGAGGCGTGGAGTGGGCGAGTTATATCATATGAGAGCACTAAATCTAGCGA 660
DB 550 GGCAGAGGCGTGGAGTGGGCGAGTTATATCATATGAGAGCACTAAATCTAGCGA 609

QY 661 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAGCACTGATCTTA 720
DB 610 GACTCCGTGAGAGGCGGATTCACATCTCCAGAGCACTTCCAGAGCACTGATCTTA 669

QY 721 AAAATGACAGCCTGAGAACTGAGAGCACGCGCTGTCTATTACTGTGCGAGATCAGAGC 780
DB 670 AAAATGACAGCCTGAGAACTGAGAGCACGCGCTGTCTATTACTGTGCGAGATCAGAGC 729

QY 781 CTGTTGGGAGCTATGACCACTACTACGTTTGAAGTCTGGGCGCAAGGAGCAGAGTC 840
DB 730 CTGTTGGGAGCTATGACCACTACTACGTTTGAAGTCTGGGCGCAAGGAGCAGAGTC 789

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DB 790 ACCGTCCTCTCAGATCCGAGCAAAAACCTGATCAGGAGAGATCTGAACATCACTCA 849

QY 901 CACCATTAAGTGAAGCTT 918
DB 850 CACCATTAAGTGAAGCTT 867

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Job time : 2906 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 17, 2003, 03:07:19 ; Search time 277 Seconds
(without alignments)
2799.666 Million cell updates/sec

Title: US-08-657-449-13

Perfect score: 918
Sequence: 1 GAATTCATGMAAAACCGC.....ATCACCATTAGTGAAGCTT 918

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 607968 segs, 422389675 residues

Total number of hits satisfying chosen parameters: 1215936

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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- 2: /cgn2_6/prodata/1/pna/US06_NEW_COMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	918	100.0	918	5	US-09-194-164-13 Sequence 13, Appl
2	916.4	99.8	918	5	US-09-194-164-15 Sequence 15, Appl
3	799.6	87.1	867	5	US-09-194-164-16 Sequence 16, Appl
4	798	86.9	867	5	US-09-194-164-18 Sequence 18, Appl
5	457	49.8	1103	1	PCT-US03-14964-4 Sequence 4, Appl
6	361	39.3	450	5	US-09-194-164-6 Sequence 6, Appl
7	359.4	39.2	450	5	US-09-194-164-4 Sequence 4, Appl
8	324.4	35.3	543	5	US-09-194-164-1 Sequence 1, Appl
9	324.4	35.3	543	5	US-09-194-164-3 Sequence 3, Appl
10	318.4	34.7	1680	1	PCT-US03-26232-15 Sequence 15, Appl
11	283.8	30.9	436	1	PCT-US03-21304-42 Sequence 42, Appl
12	282.8	30.8	324	1	PCT-US03-21304-4 Sequence 4, Appl
13	278.2	30.3	646	5	US-09-194-164-2 Sequence 2, Appl
14	274.6	29.9	351	1	PCT-US03-21304-4 Sequence 4, Appl
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16	274.6	29.9	351	1	PCT-US03-21304-6 Sequence 6, Appl
17	273.8	29.8	352	1	PCT-US03-25161-17 Sequence 17, Appl
18	273	29.7	351	1	PCT-US03-21304-7 Sequence 7, Appl
19	272.2	29.7	351	1	PCT-US03-21304-8 Sequence 8, Appl
20	271.4	29.6	324	1	PCT-US03-21304-43 Sequence 43, Appl
21	271.4	29.6	351	1	PCT-US03-21304-9 Sequence 9, Appl
22	270.6	29.5	351	1	PCT-US03-21304-10 Sequence 10, Appl
23	270.6	29.5	648	1	PCT-US03-10749A-47 Sequence 47, Appl
24	267.4	29.1	457	1	PCT-US03-26232-75 Sequence 75, Appl
25	267.4	29.1	648	1	PCT-US03-10749A-51 Sequence 51, Appl
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35	248.6	27.1	327	1	PCT-US03-10749A-23 Sequence 23, Appl
36	248.6	27.1	345	1	PCT-US03-21304-14 Sequence 14, Appl
37	248	27.0	318	1	PCT-US03-21304-46 Sequence 46, Appl
38	246.6	26.9	903	6	US-10-375-356A-12 Sequence 12, Appl
39	246.6	26.9	913	6	US-10-375-356A-10 Sequence 10, Appl
40	245.6	26.8	1430	1	PCT-US02-26584-1 Sequence 1, Appl
41	245.4	26.7	327	1	PCT-US03-10749A-27 Sequence 27, Appl
42	244.4	26.6	321	1	PCT-US03-21304-45 Sequence 45, Appl
43	244	26.6	324	1	PCT-US03-21304-48 Sequence 48, Appl
44	243.8	26.6	327	1	PCT-US03-10749A-7 Sequence 7, Appl
45	242.2	26.4	327	1	PCT-US03-10749A-15 Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-194-164-13
Sequence 13, Application US/09194164

GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Malti, Pradip K.
Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,164
FILING DATE: 09-Apr-1999
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/657,449
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 918 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
NAME/KEY: CDS
LOCATION: join(1..906, 913..918)
SEQUENCE DESCRIPTION: SEQ ID NO: 13:


```

OY 361 ACACCTCAGATCACTTTGGCGGAGAGACCAAGGTTGGAGATCAAAACGAACCTGGCTGCA 420
Db 558 ACACTCAGATCACTTTGGCGGAGAGACCAAGGTTGGAGATCAAAACGAACCTGGCTGCA 499
OY 421 CCATCTGTCTCTGGCGGTGGCGGTTCCGGAGGTGGATCATGCTGGAGGTGCTCCAG 480
Db 498 CCATCTGTCTCTGGCGGTGGCGGTTCCGGAGGTGGATCATGCTGGAGGTGCTCCAG 439
OY 481 GTGACGCTGGTGGAGATCTTGGGGGAGCGGTGTCAGACCTGGGAGGTCTCTGAGACTCTCC 540
Db 438 GTGACGCTGGTGGAGATCTTGGGGGAGCGGTGTCAGACCTGGGAGGTCTCTGAGACTCTCC 379
OY 541 TGTGAGGCTCTGGAATTCCTCCCTTCAGAAAGCTTTGCTATGCACTGGGTCGCGAGGCTCTA 600
Db 378 TGTGAGGCTCTGGAATTCCTCCCTTCAGAAAGCTTTGCTATGCACTGGGTCGCGAGGCTCTA 319
OY 601 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATATATGATGAGAGCACTAAATATCAACGA 660
Db 318 GGCAAGGGGCTGGAGTGGGTGGCAGTTATATATATGATGAGAGCACTAAATATCAACGA 259
OY 661 GATTCCTGGAAAGGCGCGATTCACCATCTTCCAGAGACATTCCAAGAACCGGTGATCTA 720
Db 258 GATTCCTGGAAAGGCGCGATTCACCATCTTCCAGAGACATTCCAAGAACCGGTGATCTA 199
OY 721 AAAATGACAGGCTTGAGACTGAGACACAGCGCTGCTATTACTGTGCGAGAGATCAGAC 780
Db 198 AAAATGACAGGCTTGAGACTGAGACACAGCGCTGCTATTACTGTGCGAGAGATCAGAC 139
OY 781 CTGTTGGTGACTATGACCACTACTACGCTTTGACGCTTGGGGCAAAAGGACCAAGCTC 840
Db 138 CTGTTGGTGACTATGACCACTACTACGCTTTGACGCTTGGGGCAAAAGGACCAAGCTC 79
OY 841 ACCGCTCTCAGAGATCCGGAACAAACCTGATCAACGAAAGATCTGAACCATCAACCT 900
Db 78 ACCGCTCTCAGAGATCCGGAACAAACCTGATCAACGAAAGATCTGAACCATCAACCT 19
OY 901 CACCATTAGTGAAGCTT 918
Db 18 CACCATTAGTGAAGCTT 1

RESULT 3
US-09-194-164-16
; Sequence 16, Application US/09194164
; GENERAL INFORMATION:
; APPLICANT: Dan, Michael D.
; Maiti, Pradipt K.
; Kaplan, Howard A.
; TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
; SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
; FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
; DETECTION OF CANCERS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morrison & Foerster
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/194.164
; FILING DATE: 09-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,449
; FILING DATE: <Unknown>

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Query	Match	Best Local Similarity	Matches	Score	DB	Length	Indels	Gaps
QY	1	94.0%	863	799.6	5	867	4	1
Db	1							
QY	61							
Db	61							
QY	121							
Db	121							
QY	181							
Db	181							
QY	241							
Db	241							
QY	301							
Db	301							
QY	361							
Db	361							
QY	421							
Db	421							
QY	481							
Db	481							
QY	541							
Db	541							
QY	601							
Db	601							
QY	661							
Db	661							
QY	721							
Db	721							

Db 670 AAATGAAGAGCTGAGAACTGAGACACGCGTGTCTATTACTGTGCGAGAGTCAAGAC 729
Qy 781 CTGTGGGTGACATATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCTC 840
Db 730 CTGTGGGTGACATATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCTC 789
Qy 841 ACCGTCCTCAGAGATCCGAAACAAATGATCAGGAGAGATCTGAACATCAACAT 900
Db 790 ACCGTCCTCAGAGATCCGAAACAAATGATCAGGAGAGATCTGAACATCAACAT 849
Qy 901 CACCATTAAGTGAAGCTT 918
Db 850 CACCATTAAGTGAAGCTT 867

RESULT 4
US-09-194-164-18/c
Sequence 18, Application US/09194164
GENERAL INFORMATION:
APPLICANT: Dan, Michael D.
Maifi, Pradiip K.
Kaplan, Howard A.
TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESS: Morrison & Foerster
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/194,164
FILING DATE: 09-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/657,449
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lehnhardt, Susan K.
REGISTRATION NUMBER: 33,943
REFERENCE/DOCKET NUMBER: 31608-20001.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-194-164-18

Query Match 86.9%; Score 798; DB 5; Length 867;
Best Local Similarity 93.9%; Pred. No. 5,4e-223;
Matches 862; Conservative 0; Mismatches 5; Indels 51; Gaps 1;

Qy 1 GAATTCATGAAAAAACCCTATCCGATCCGAGTGGACCTGCTGCTTCCCTACCGT 60
Db 867 GAATTCATGAAAAAACCCTATCCGATCCGAGTGGACCTGCTGCTTCCCTACCGT 808
Qy 61 GGCGAGCGCATTTGTGTGACGAGTCTCCAGGACCCCTGTTTGTCTCCAGGGGAA 120

Db 807 GGCGAGCGCATTTGTGTGACGAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAA 748
Qy 121 AGAGCCACCTCTCTCCGAGGGCCAGTCAAGTGTGTATGACACTTATGACCTGATC 180
Db 747 AGAGCCACCTCTCTCCGAGGGCCAGTCAAGTGTGTATGACACTTATGACCTGATC 688
Qy 181 CAGCGAAACCTGGCGAGGCTCCAGGCTCTCATCTATGATGATCCACAGGGGCACT 240
Db 687 CAGCGAAACCTGGCGAGGCTCCAGGCTCTCATCTATGATGATCCACAGGGGCACT 628
Qy 241 GGCGATCCGAGCAGGTTGAGTGGAGTGGTCCGGGACAGACTTCACTTCAACATCAT 300
Db 627 GGCGATCCGAGCAGGTTGAGTGGAGTGGTCCGGGACAGACTTCACTTCAACATCAT 568
Qy 301 AGACTGAGCTGAAAGATTTTGCAGTGTATTAATCTGTGAGAGTATGAGTCACTGAG 360
Db 567 AGACTGAGCTGAAAGATTTTGCAGTGTATTAATCTGTGAGAGTATGAGTCACTGAG 508
Qy 361 ACACCTCAGATCACTTTCGCGAGGAGGACCAAGTGGAGATCAACAGAACTGGCTGCA 420
Db 507 ACACCTCAGATCACTTTCGCGAGGAGGACCAAGTGGAGATCAACAGAACTGGCTGCA 448
Qy 421 CCATCTGTCTTGGCGGTGGCGGTCCGAGGTGGATCAGTGGAGTGGCTCCAG 480
Db 447 TC-----CGAGCAG 439
Qy 481 GTGCGAGTGTGAGTCTGGGGGAGCGTGTCCAGCCTGGAGGCTCCAGACTCC 540
Db 438 GTGCGAGTGTGAGTCTGGGGGAGCGTGTCCAGCCTGGAGGCTCCAGACTCC 379
Qy 541 TGTGAGCTCTGAGATTCCTTCAAGACTTGTGATGACCTGGTCCGAGCTCTA 600
Db 378 TGTGAGCTCTGAGATTCCTTCAAGACTTGTGATGACCTGGTCCGAGCTCTA 319
Qy 601 GGCGAGGCTGTGAGTGGTGGTGGTGTATATATATGATGAAAGCACTAAATATACGCA 660
Db 318 GGCGAGGCTGTGAGTGGTGGTGGTGTATATATATGATGAAAGCACTAAATATACGCA 259
Qy 661 GATCGGTGAAAGGCGGATTCACCATCTCCAGAGCACTTCCAGAAACGCGTGTATCTA 720
Db 258 GATCGGTGAAAGGCGGATTCACCATCTCCAGAGCACTTCCAGAAACGCGTGTATCTA 199
Qy 721 AAATGAAGAGCTGAGAACTGAGACACGCTGTCTATTACTGTGCGAGATCAAGAC 780
Db 198 AAATGAAGAGCTGAGAACTGAGACACGCTGTCTATTACTGTGCGAGATCAAGAC 139
Qy 781 CTGTGGGTGACATATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCTC 840
Db 138 CTGTGGGTGACATATGACCACTACTACGTTTGAAGTCTGGGGCAAGGAGCAAGCTC 79
Qy 841 ACCGTCCTCAGAGATCCGAAACAAATGATCAGGAGAGATCTGAACATCAACAT 900
Db 78 ACCGTCCTCAGAGATCCGAAACAAATGATCAGGAGAGATCTGAACATCAACAT 19
Qy 901 CACCATTAAGTGAAGCTT 918
Db 18 CACCATTAAGTGAAGCTT 1

RESULT 5
PCT-US03-14964-4
Sequence 4, Application PC/TUS0314964
GENERAL INFORMATION:
APPLICANT: Rother, Russell P
Geis, David R
TITLE OF INVENTION: T7 Bacteriophage Display of Fabs
FILE REFERENCE: 1087-24 PCT
CURRENT APPLICATION NUMBER: PCT/US03/14964
CURRENT FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: US 60/380,318
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 16

SOFTWARE: PatentIn version 3.2
 SEQ ID NO 4
 LENGTH: 1103
 TYPE: DNA
 ORGANISM: human
 PCT-US03-14964-4

Query Match 49.8%; Score 457; DB 1; Length 1103;
 Best Local Similarity 74.3%; Pred. No. 2.1e-123;
 Matches 628; Conservative 0; Mismatches 190; Indels 27; Gaps 3;

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QY 7 ATGAAAAAACCGCTATCCGATCGCATGTCCTGGCTGGTTCCCTACCGTGGCAG 66
DB 210 ATGAAAAAACAGCTATCCGATGAGGCACTGGCTGGTTCCCTACCGTGGCAG 269
QY 67 GCGATATGTTGTCAGGAGTCTCCAGGCACTGCTGTTGTCCTCAGGGGAAAGAGCC 126
DB 270 GCGG---CCGAGCTACGAGTCTCCAGGCACTGCTGTTGTCCTCAGGGGAAAGAGCC 326
QY 127 ACCCTCTCTGCAAGGCGCAGTCAGAGTGTAGAGAGCTACTTACCTGTACAGCAG 186
DB 327 ACCCTCTCTGCAAGGCGCAGTCAGAGTGTAGAGAGCTACTTACCTGTACAGCAG 386
QY 187 AAACCTGGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACTGGCAGT 246
DB 387 AAACCTGGCAGGCTCCAGGCTCTCATCTATGTCATCCACAGGGCCACTGGCAGT 446
QY 247 CCAGACAGGTTGAGTGGCAGTGGGTCGGGAGCAGCTTCACTCTCAGTCAGTAGAGT 306
DB 447 CCAGACAGGTTGAGTGGCAGTGGGTCGGGAGCAGCTTCACTCTCAGTCAGTAGAGT 506
QY 307 GAGCCTGAAGATTTGTCAGTGTATTACTGTACAGCAGTATGAGTCACTCAGACAG 366
DB 507 GAGCCTGAAGATTTGTCAGTGTATTACTGTACAGCAGTATGAGTCACTCAGACAG 560
QY 367 CAGATCACTTTGGCGGAGGAGCAGAGTGTAGATCAAGCACTGTGGCTGCACATCT 426
DB 561 -----TTGCGGCCAGAGGAGCAGAGTGTAGATCAAGCACTGTGGCTGCACATCT 611
QY 427 GTCTGTGGGCGGTGGCGGTTCCGAGGTGGTGCAGTGGTGGCTCCAGAGTGCAG 486
DB 612 GCTGTGGGCGGTGGCGGTTCCGAGGTGGTGCAGTGGTGGCTCCAGAGTGCAG 662
QY 487 CTGTCAGTCTGTGGGAGGAGCGGTGTCCAGCCTGGAGAGTCCCTGAGACTCTCTGTGA 546
DB 663 CTGTCAGTCTGTGGGAGGAGCGGTGTCCAGCCTGGAGAGTCCCTGAGACTCTCTGTGA 722
QY 547 GCTTCGTGATTCCTTCAGAACTTTGCTATGCACTGGGTCGCGAGGCTCTAGGCAAG 606
DB 723 GCTTCGTGAGGCACTTCAGAACTTTGCTATGCACTGGGTCGCGAGGCTCTAGGCA 782
QY 607 GGGCTGAGTGGGTGGCAGTATATCATATGATGAGAGCACTAAATCAACGAGCTCC 666
DB 783 GGGCTGAGTGGGTGGCAGTATATCATATGATGAGAGCACTAAATCAACGAGCTCC 842
QY 667 GTGAAGGCGGATTCACATCTCCAGAGACACTTCCAGAGACGCGTGTATCTAAATG 726
DB 843 TTCCAGGGGAGAGTACCATTCACCGGAGAGATCCACGGGCAACCTCAATGAGCTG 902
QY 727 AACAGCTTAGAACTGAGAGCAACGCGTGTCTATTACTGTGCGAGAGATCAAGCTGTG 786
DB 903 AACAGCTTAGAACTGAGAGCAACGCGTGTCTATTACTGTGCGAGAGATCAAGCTGTG 962
QY 787 GGTGACTATGACCACTACGTTTGGAGCTGTGGGCGAAAGGAGCAACGCTCAACCTG 846
DB 963 GGTGACTATGACCACTACGTTTGGAGCTGTGGGCGAAAGGAGCAACGCTCAACCTG 1022
QY 847 TCCTC 851
DB 1023 TCAC 1027

```

RESULT 6

US-09-194-164-6/c
 Sequence 6, Application US/09194164
 GENERAL INFORMATION:
 APPLICANT: Dan, Michael D.
 Maltl, Pradip K.
 Kaplan, Howard A.
 TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS
 NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA
 COUNTRY: USA
 ZIP: 94304-1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/194,164
 FILING DATE: 09-Apr-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/657,449
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Leinhardt, Susan K.
 REGISTRATION NUMBER: 33,943
 REFERENCE/DOCKET NUMBER: 31608-20001.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792
 TELE: 706141
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 450 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
 US-09-194-164-6

Query Match 39.3%; Score 361; DB 5; Length 450;
 Best Local Similarity 100.0%; Pred. No. 1.6e-95;
 Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 70 GATATTTGTTGACGACAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAAAGACCCAC 129
DB 378 GATATTTGTTGACGACAGTCTCCAGGACCCCTGTTGTCTCCAGGGGAAAGACCCAC 319
QY 130 CTCTCTCAGGGGCGAGTCAGAGTGTAGTACAGTACTTAGCTGTGATCCAGAGAA 189
DB 318 CTCTCTCAGGGGCGAGTCAGAGTGTAGTACAGTACTTAGCTGTGATCCAGAGAA 259
QY 190 CTTGACAGGCTCCAGGCTCTCATCTATGAGTGCATCCAGGAGCCACTGGATGCCA 249
DB 258 CTTGACAGGCTCCAGGCTCTCATCTATGAGTGCATCCAGGAGCCACTGGATGCCA 199
QY 250 GACAGTTCAGTGGAGTGGTCCGGGACAGACTTCACTCTCAACATAGTAGACTGGAG 309
DB 198 GACAGTTCAGTGGAGTGGTCCGGGACAGACTTCACTCTCAACATAGTAGACTGGAG 139
QY 310 CCTGAAGATTTGACAGTGTATTAAGTACAGCAGTATGAGTCACTCAGACCTGAG 369
DB 138 CCTGAAGATTTGACAGTGTATTAAGTACAGCAGTATGAGTCACTCAGACCTGAG 79
QY 370 ATCACTTTGCGGAGGAGCAAGGTGAGATCAAGCACTGTGGCTGACCATCTGTC 429

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Db 78 ATCACTTTCGGCGAGGACCAAGGTGAGATCAAGCACTGTCGACCATCTGTC 19
QY 430 T 430
Db 18 T 18

RESULT 7

US-09-194-164-4

Sequence 4, Application US/09194164
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Malti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194.164

FILING DATE: 09-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/657.449

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 450 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..450

SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-194-164-4

Query Match 39.2%; Score 359.4; DB 5; Length 450;

Best Local Similarity 99.7%; Pred. No. 4,7e-95;

Matches 360; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 70 GATATTGTGTGAGCGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGGCCACC 129

Db 73 GATATTGTGTGAGCGAGTCTCCAGGACCCCTGCTTGTCTCCAGGGGAAAGGCCACC 132

QY 130 CTCTCTGCGAGGGCGCACTGAGGTGTTAGTAGAGCTACTTACCTGCTGTAACGAGGAAA 189

Db 133 CTCTCTGCGAGGGCGCACTGAGGTGTTAGTAGAGCTACTTACCTGCTGTAACGAGGAAA 192

QY 190 CCTGGCGAGGCTCCCGAGGCTCTCATATAGTGTCATCCACCGAGGCGCACTGGCATGCCA 249

Db 193 CCTGGCGAGGCTCCCGAGGCTCTCATATAGTGTCATCCACCGAGGCGCACTGGCATGCCA 252

QY 250 GACAGGTTACGTGCGAGTGGTCCGAGACACTTCACTCTCAACCATGAGTAAGCTGGAG 309
Db 253 GACAGGTTACGTGCGAGTGGTCCGAGACACTTCACTCTCAACCATGAGTAAGCTGGAG 312
QY 310 CTTGAGATTGTCAGTGTATCTGTCAGCACTATGTTAGTCTCACTCTGAGACCTCGAG 369
Db 313 CTTGAGATTGTCAGTGTATCTGTCAGCACTATGTTAGTCTCACTCTGAGACCTCGAG 372
QY 370 ATCACTTTCGGCGAGGACCAAGGTGAGATCAAGCACTGTGCTGACCATCTGTC 429
Db 373 ATCACTTTCGGCGAGGACCAAGGTGAGATCAAGCACTGTGCTGACCATCTGTC 432
QY 430 T 430
Db 433 T 433

RESULT 8

US-09-194-164-1

Sequence 1, Application US/09194164
GENERAL INFORMATION:

APPLICANT: Dan, Michael D.

Malti, Pradip K.

Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT
SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster

STREET: 755 Page Mill Road

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/194.164

FILING DATE: 09-Apr-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/657.449

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.

REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600

TELEFAX: (415) 494-0792

TELEX: 706141

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 543 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURE:

NAME/KEY: CDS

LOCATION: 1..543

SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-09-194-164-1

Query Match 35.3%; Score 324.4; DB 5; Length 543;

Best Local Similarity 89.3%; Pred. No. 8.4e-85;

Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGAGTGTGATCAGGTGAGAGTGGCTCCAGAGTCCAGCTGTGTGAGTCTG 499
 DB 152 GGGTTTCTCTGCTGTCTTTTAAGAGTATCCAGGTGATGAGTGGAGTGTGAGTCTG 211
 QY 500 GGGGAGGCGGTGATCCAGCTGTGAGAGTCCCTGAGACTCTCTGTGAGCTCTGAGATTCC 559
 DB 212 GGGGAGGCGGTGATCCAGCTGTGAGAGTCCCTGAGACTCTCTGTGAGCTCTGAGATTCC 271
 QY 560 CCTTCAGAGCTTTGCTATGCACTGGGTCGCGCAGGCTCTAGGCAAGGGCTGAGTGGG 619
 DB 272 CTTTCAAGAGCTTTGCTATGCACTGGGTCGCGCAGGCTCTAGGCAAGGGCTGAGTGGG 331
 QY 620 TGGCAGTTATATCATATGATGAGACATAAATACTAGCAGACTCTCTGTGAGAGCCGAT 679
 DB 332 TGGCAGTTATATCATATGATGAGACATAAATACTAGCAGACTCTCTGTGAGAGCCGAT 391
 QY 680 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATTAATAAATGAACAGCTGAGAA 739
 DB 392 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATTAATAAATGAACAGCTGAGAA 451
 QY 740 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATCAGAGCTGTGGTGAATAAGCC 799
 DB 452 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATCAGAGCTGTGGTGAATAAGCC 511
 QY 800 ACTACTACGAGTTGAGAGTCTGGGAGCAAGG 830
 DB 512 ACTACTACGAGTTGAGAGTCTGGGAGCAAGG 542

RESULT 9

US-09-194-164-3/c
 ; Sequence 3, Application US/09194164
 ; GENERAL INFORMATION:

APPLICANT: Dan, Michael D.
 Malet, Pradip K.
 Kaplan, Howard A.

TITLE OF INVENTION: ANTIGEN BINDING FRAGMENTS THAT SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND DETECTION OF CANCERS

NUMBER OF SEQUENCES: 18
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Morrison & Foerster
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: CA

COUNTRY: USA
 ZIP: 94304-1018

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Releasee #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/194,164

FILING DATE: 09-Apr-1999
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/657,449

FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:

NAME: Lehnhardt, Susan K.
 REGISTRATION NUMBER: 33,943

REFERENCE/DOCKET NUMBER: 31608-20001.00
 TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 813-5600
 TELEFAX: (415) 494-0792

TELEX: 706141
 INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
 LENGTH: 543 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double

TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
 ; US-09-194-164-3

Query Match 35.3%; Score 324.4; DB 5; Length 543;
 Best Local Similarity 89.3%; Pred. No. 8,4e-85;
 Matches 349; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 440 GCGGTTCCGAGAGTGTGATCAGGTGAGAGTGGCTCCAGAGTCCAGCTGTGTGAGTCTG 499
 DB 392 GGGTTTCTCTGCTGTCTTTTAAGAGTATCCAGGTGATGAGTGGAGTGTGAGTCTG 333
 QY 500 GGGGAGGCGGTGATCCAGCTGTGAGAGTCCCTGAGACTCTCTGTGAGCTCTGAGATTCC 559
 DB 332 GGGGAGGCGGTGATCCAGCTGTGAGAGTCCCTGAGACTCTCTGTGAGCTCTGAGATTCC 273
 QY 560 CCTTCAGAGCTTTGCTATGCACTGGGTCGCGCAGGCTCTAGGCAAGGGCTGAGTGGG 619
 DB 272 CTTTCAAGAGCTTTGCTATGCACTGGGTCGCGCAGGCTCTAGGCAAGGGCTGAGTGGG 213
 QY 620 TGGCAGTTATATCATATGATGAGACATAAATACTAGCAGACTCTCTGTGAGAGCCGAT 679
 DB 212 TGGCAGTTATATCATATGATGAGACATAAATACTAGCAGACTCTCTGTGAGAGCCGAT 153
 QY 680 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATTAATAAATGAACAGCTGAGAA 739
 DB 152 TCACCATCTCCAGAGACACTTCCAGAGACAGGTGTATTAATAAATGAACAGCTGAGAA 93
 QY 740 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATCAGAGCTGTGGTGAATAAGCC 799
 DB 92 CTGAGAGACAGGCTGTCTATTACTGTGCGAGAGATCAGAGCTGTGGTGAATAAGCC 33
 QY 800 ACTACTACGAGTTGAGAGTCTGGGAGCAAGG 830
 DB 32 ACTACTACGAGTTGAGAGTCTGGGAGCAAGG 2

RESULT 10

PCT-US03-14964-1
 ; Sequence 1, Application PC/TUS0314964

GENERAL INFORMATION:

APPLICANT: Rother, Russell P
 APPLICANT: Geis, David R

TITLE OF INVENTION: T7 Bacteriophage Display of Fabs
 FILE REFERENCE: 1087-24 PCT

CURRENT APPLICATION NUMBER: PCT/US03/14964
 CURRENT FILING DATE: 2003-07-17

PRIOR APPLICATION NUMBER: US 60/380,318
 PRIOR FILING DATE: 2002-05-14

NUMBER OF SEQ ID NOS: 16
 SOFTWARE: Patentin version 3.2

SEQ ID NO 1

LENGTH: 1680
 TYPE: DNA
 ORGANISM: human

PCT-US03-14964-1
 Query Match 34.7%; Score 318.4; DB 1; Length 1680;
 Best Local Similarity 88.4%; Pred. No. 7,2e-83;

Matches 375; Conservative 0; Mismatches 31; Indels 18; Gaps 2;

QY 7 ATGAAAAAACCGCATCGCATCGCATGTCGCTGTTGCGTACCGTGGCGAG 66
 DB 7 ATGAAAAAACCGCATCGCATCGCATGTCGCTGTTGCGTACCGTGGCGAG 66
 QY 67 GCGGATTTGTTGATGAGAGTCTCCAGGACCTGTCTTTGTCTCCAGGAGAAAGAGCC 126
 DB 67 GCGGATTTGTTGATGAGAGTCTCCAGGACCTGTCTTTGTCTCCAGGAGAAAGAGCC 123
 QY 127 ACCCTCTCTGAGGAGCAGTGAAGTGTATACAGTCTTGGTGGTACGAGCAG 186
 DB 127 ACCCTCTCTGAGGAGCAGTGAAGTGTATACAGTCTTGGTGGTACGAGCAG 183

QY	187	AAACCTGGCAGAGCTCCAGGGCTCCATCTATAGTGCATCCACGAGGGCAGTGGCAGT	246
Db	184	AAACTGGCAGAGCTCCAGGCTCTCATCTATAGTGCATCCAGGGCAGTGGCAGT	243
QY	247	CCAGACAGGTTCAGTGGCAGTGGGTCGGGACAGACTTCACTCTCAACATCAGTAGACTG	306
Db	244	CCAGACAGGTTCAGTGGCAGTGGGTCGGGACAGACTTCACTCTCAACATCAGTAGACTG	303
QY	307	GAGCCTGAAGATTTTGCAGTGTATTACTGTACACAGTATAGTAGCTCACTCAGACACT	366
Db	304	GAGCCTGAAGATTTTGCAGTGTATTACTGTACACAGTATAGTAGCTCACTCAGACACT	357
QY	367	CAGATCACTTTCGGCGAGAGGACCAAGTGTGATCAACGAAGTGGCTGCACCATCT	426
Db	358	-----TTGGGCCAAGGACCAAGGTGAAGCTCAAGAACTGTGGCTGCACCATCT	408
QY	427	GTCT	430
Db	409	GTCT	412

```

RESULT 11
PCT-US03-26232-145
; Sequence 145, Application PC/TUS0326232
; GENERAL INFORMATION:
; APPLICANT: ABGENIX, INC.
; APPLICANT: GUDAS, Jean M.
; APPLICANT: HAAK-FRENDSCHO, Mary
; APPLICANT: FOORD, Orit
; APPLICANT: LIANG, Meina L.
; APPLICANT: AHLUMWALIA, Kiran
; APPLICANT: BHAKTA, Sunil
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO MONOCYTE
; TITLE OF INVENTION: CHEMO-ATTRACTANT PROTEIN-1 (MCP-1) AND USES THEREOF
; FILE REFERENCE: ABGENIX_091VPC
; CURRENT APPLICATION NUMBER: PCT/US03/26232
; CURRENT FILING DATE: 2003-08-19
; PRIOR APPLICATION NUMBER: US 60/404,802
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 436
; TYPE: DNA
; ORGANISM: Homosapien
PCT-US03-26232-145

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Query Match	30.9%	Score 293.8	DB 1	Length 436
Best Local Similarity	88.1%	Pred No.5-73		
Matches 325	Conservative 0	Mismatches 32	Indels 12	Gaps 1

Qy	430	GTGAGCTCTGGGGAGAGCGTGTGCAGCCCTGGAGGCTCCCTGAGACTCTCTGTGTGCAGCC	549
Db	1	GAGCAGTCCGGGGGGAGAGCGTGTGCAGCTGGGAGTCCCTGAGACTCTCTGTGCAGCG	60
Qy	550	TCTGGATTCCTCCCTTGAGAACTTTTGTCTATGCACTGGGTCCGCGAAGCTCTAAGGCAAGGG	609
Db	61	TCTGATTTCACTTACGTAGTGTATGGACATGCACTGGTCCGCGAAGCTCTCCAGCAAGGG	120
Qy	610	CTGGAGTGGGTGGCAGTTATATCATATGATGAGAACACTAAATACCTACGACAGCTCCGTG	669
Db	121	CTGGAGTGGGTGGCAGTTATATGATATGATGAGAAATTAATTAATCTAAGCAGACTCCGTG	180
Qy	670	AAGGCCCGATTTCACATCTCCGAGAACACTTCCAAAGAACGSGTGTATCTAAATTAAGAC	729
Db	181	AAGGCCCGATTTCACATCTCCGAGAACACTTCCAAAGAACCGCTGTATCTGCAATTAAGAC	240
Qy	730	AGCTGAGAACTGAGAGACAGCGCTGTCTATTACTGCGAGAGATCAGAGCCTGTGGGT	789
Db	241	AGCTGAGAGCCGAGAGACAGCGCTGTCTATTACTGCGAGAGATAGCAGCTGTG-----	295
Qy	790	GACTATGACCACTACTACGGTTTGACGCTTGGGGCAAGGAGACACGGTCAACCGTCTCC	849

Db 256 -----ACTTACTACTACGGATGACGCTTGGGGCCAAAGGACACACGGTCAACCGTCTCC 348

QY 850 TCAGGATCC 858
|||
|||

Db 349 TCAGGCTCC 357

```

RESULT 12
PCT-US03-21304-42
; Sequence 42, Application PC/TUS0321304
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
; FILE REFERENCE: 053893-5050MO
; CURRENT APPLICATION NUMBER: PCT/US03/21304
; CURRENT FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/394,356
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 60/411,694
; PRIOR FILING DATE: 2003-09-18
; NUMBER OF SEQ ID NOS: 153
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 42
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US03-21304-42

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[illegible]

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RESULT 13
US-09-610-551B-2
; Sequence 2, Application US/09610551B
;
; GENERAL INFORMATION:
;
; APPLICANT: Barbas, Carlos F, III
;
; Burton, Dennis R
;
; Lerner, Richard A
;
; TITLE OF INVENTION: METHODS FOR PRODUCING ANTIBODY LIBRARIES
;
; USING UNIVERSAL OR RANDOMIZED IMMUNOGLOBULIN LIGHT CHAINS
;
;
; NUMBER OF SEQUENCES: 70
;
; CORRESPONDENCE ADDRESS:
;
; ADDRESSEE: The Scripps Research Institute
;
; STREET: 10666 North Torrey Pines Road, TPC8
;
; CITY: La Jolla
;
; STATE: CA
;

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COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/610,551B
FILING DATE: 05-Jul-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/826,623
FILING DATE: 27-JAN-1992
APPLICATION NUMBER: US 08/174,674
FILING DATE: 28-DEC-1993
APPLICATION NUMBER: US 08/300,386
FILING DATE: 02-SEP-1994
APPLICATION NUMBER: US 08/931,645
FILING DATE: 16-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Fitting, Thomas
REGISTRATION NUMBER: 34,163
REFERENCE/DOCKET NUMBER: TSRI 409.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 858-554-2937
TELEFAX: 858-554-6312
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 646 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-610-551B-2

Query Match      30.3%; Score 278.2; DB 5; Length 646;
Best Local Similarity 89.3%; Pred. No. 2,7e-71;
Matches 317; Conservative 0; Mismatches 23; Indels 15; Gaps 1;

QY 76 GTGTGACGACGCTTCACGACACCCCTGTTGTCTCCAGGGGAAAGACCCCTCTCC 135
DB 1 GAGCTCAGCAGCTTCACGACACCCCTGTTGTCTCCAGGGGAAAGACCCCTCTCC 60
QY 136 TCCAGGGCCAGTCAAGTGTAGTACAGCTACTTACCTGGTACCAAGAAAGCTGGC 195
DB 61 TCCAGGGCCAGTCAAGTGTAGTACAGGGGCTTACTTACCTGGTACCAAGAAAGCTGGC 120
QY 196 CAGGCTCCAGGCTCCTCATCTATGTTGATGATCCACAGGGGCACTGGCAGACAG 255
DB 121 CAGGCTCCAGGCTCCTCATCTATGTTGATGATCCACAGGGGCACTGGCAGACAG 180
QY 256 TTCAAGTGCAGTGTCCGCGACAGACTTCACTCTCCACCATGAGTACAGCTGGA 315
DB 181 TCCAGTGGAGTGGGTCTGGACAGACTTCACTCTCCACCATGAGTACAGCTGGA 240
QY 316 GATTTTGACGTATTAATCTGTCAAGCAGTATGTTAGCTTCACTCAGACACCTCAATCACT 375
DB 241 GATTTTGACGTATTAATCTGTCAAGCAGTATGTTAGCTTCACTCAGACACCTCAATCACT 285
QY 376 TTCCGGCGAGGACCAAGGTGAGATCAAGCAAGTGGCTGACCATCTGTCT 430
DB 286 TTCCGGCGAGGACCAAGGTGAGATCAAGCAAGTGGCTGACCATCTGTCT 340

RESULT 14
PCT-US03-21304-4
Sequence 4: Application PC/TUS0321304
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
FILE REFERENCE: 053893-5050WO
CURRENT APPLICATION NUMBER: PCT/US03/21304
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/394,356
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/411,694
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-21304-5

Query Match      29.9%; Score 274.6; DB 1; Length 351;
Best Local Similarity 95.3%; Pred. No. 2,5e-70;
Matches 283; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 478 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTC 537
DB 1 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTC 60
QY 538 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTATGACATGGGTCCGAGGCT 597
DB 61 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTATGACATGGGTCCGAGGCT 120
QY 598 CTAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGANGAAGCACTAATATCTAC 657
DB 121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGANGAAGCACTAATATCTAC 180
QY 658 GCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACCTCCAGAAACAGGGGTAT 717
DB 181 GCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACCTCCAGAAACAGGGGTAT 240
QY 718 CTAAATGAACAGCCTGAGAACTGAGACACAGGCTGTCTATTACTGTGCGAGAGAT 774
DB 241 CTGAAATGAACAGCCTGAGAACTGAGACACAGGCTGTCTATTACTGTGCGAGAGAT 297
```

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TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
FILE REFERENCE: 053893-5050WO
CURRENT APPLICATION NUMBER: PCT/US03/21304
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/394,356
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/411,694
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PatentIn version 3.2
SEQ ID NO 4
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-21304-4

Query Match      30.1%; Score 276.2; DB 1; Length 351;
Best Local Similarity 95.6%; Pred. No. 8,4e-71;
Matches 284; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 478 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTC 537
DB 1 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTC 60
QY 538 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTATGACATGGGTCCGAGGCT 597
DB 61 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTATGACATGGGTCCGAGGCT 120
QY 598 CTAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGANGAAGCACTAATATCTAC 657
DB 121 CCAGGCAAGGGGCTGAGTGGGTGGCAGTTATATCATATGANGAAGCACTAATATCTAC 180
QY 658 GCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACCTCCAGAAACAGGGGTAT 717
DB 181 GCAGACTCCGTGAAGGCGGATTCACATCTCCAGAGACCTCCAGAAACAGGGGTAT 240
QY 718 CTAAATGAACAGCCTGAGAACTGAGACACAGGCTGTCTATTACTGTGCGAGAGAT 774
DB 241 CTGAAATGAACAGCCTGAGAACTGAGACACAGGCTGTCTATTACTGTGCGAGAGAT 297

RESULT 15
PCT-US03-21304-5
Sequence 5: Application PC/TUS0321304
GENERAL INFORMATION:
APPLICANT: Siegel, Donald L.
TITLE OF INVENTION: COMPOSITIONS, METHODS AND KITS RELATING TO ANTI-PLATELET
FILE REFERENCE: 053893-5050WO
CURRENT APPLICATION NUMBER: PCT/US03/21304
CURRENT FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/394,356
PRIOR FILING DATE: 2003-07-03
PRIOR APPLICATION NUMBER: 60/411,694
PRIOR FILING DATE: 2003-09-18
NUMBER OF SEQ ID NOS: 153
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 351
TYPE: DNA
ORGANISM: Homo sapiens
PCT-US03-21304-5

Query Match      29.9%; Score 274.6; DB 1; Length 351;
Best Local Similarity 95.3%; Pred. No. 2,5e-70;
Matches 283; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 478 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTC 537
DB 1 CAGGTGACGCTGTGAGTCTGGGGAGGCGGTGTCAGCCTGGAGAGTCCCTGAGACTC 60
QY 538 TCCGTGACGCTCTGGAATTCCTCTTCAAGACCTTGTATGACATGGGTCCGAGGCT 597
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